APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/535,500	05/26/2006	Anne Mette Buhl Hertz	55320.001041	7327

21967   7590   11/13/2007
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EXAMINER
GUSSOW, ANNE

ART UNIT	PAPER NUMBER
1643	

MAIL DATE	DELIVERY MODE
11/13/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

	Application No.	Applicant(s)
Office Action Summary	10/535,500	HERTZ ET AL.
	Examiner	Art Unit	
	Anne M. Gussow	1643	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE <u>3</u> MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.
- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
  Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on <u>20 September 2007</u>.

2a)☐ This action is **FINAL.**   2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) <u>43-60</u> is/are pending in the application.

    4a) Of the above claim(s) <u>48,51,52 and 55-60</u> is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) <u>43-47,49,50,53 and 54</u> is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on <u>18 May 2005</u> is/are: a)☒ accepted or b)☐ objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

    Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

    a)☒ All   b)☐ Some * c)☐ None of:

      1.☐ Certified copies of the priority documents have been received.

      2.☐ Certified copies of the priority documents have been received in Application No. _____.

      3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

    * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)

2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3) ☒ Information Disclosure Statement(s) (PTO/SB/08)
    Paper No(s)/Mail Date <u>11/18/05, 2/09/06</u>.

4) ☐ Interview Summary (PTO-413)
    Paper No(s)/Mail Date. _____ .

5) ☐ Notice of Informal Patent Application

6) ☒ Other: <u>Sequence alignment</u>.

DETAILED ACTION

1.   Applicant's election with traverse of Group I in the reply filed on September 20,

2007 is acknowledged. The traversal is on the ground(s) that the restriction

requirement does not conform to the PCT unity of invention rules in that lack of unity

was not found in the PCT application and the instant application is a national stage

entry of the PCT application. This is not found persuasive because while the national

and regional Offices may not make further requirements beyond those of the Treaty and

Regulations in respect of matters of form and contents, they are not bound by the

Treaty to follow the results of any international search or examination which has been

performed when the application is examined during the national or regional phase (see

International Search and Preliminary Examination Guidelines page 15 paragraph 1.12).

Therefore, for the reasons presented in the previous office action, the restriction

requirement is still deemed proper and is therefore made FINAL.

2.   Applicant's election with traverse of SEQ ID No. 11 in the reply filed on

September 20, 2007 is acknowledged. The traversal is on the ground(s) that SEQ ID

Nos. 12-18 correspond to single AMB1/CLLU1 exon sequences which never exist as

"single transcripts" and that any transcript that includes the sequence from the start of

the AMB1/CLLU1 primary transcript can be used for B-CLL diagnostics. Applicant has

requested examination of additional species should SEQ ID No. 11 be found allowable,

for the reasons set forth below SEQ ID No. 11 has not be deemed allowable and no

additional species have been searched at this time.

3.   Claims 48, 51, 52, and 55-60 are withdrawn from further consideration pursuant

to 37 CFR 1.142(b), as being drawn to a nonelected species, there being no allowable

generic or linking claim. Applicant timely traversed the restriction (election) requirement

in the reply filed on September 20, 2007.

4.   Claims 43-47, 49, 50, 53, and 54 are under examination to the extent that they

relate to SEQ ID No. 11.

Information Disclosure Statement

5.   The information disclosure statements (IDS) submitted on November 18, 2005

and February 9, 2006 have been fully considered by the examiner and an initialed copy

of the IDS is included with the mailing of this Office Action.

6.   The listing of references in the specification is not a proper information disclosure

statement. 37 CFR 1.98(b) requires a list of all patents, publications, or other

information submitted for consideration by the Office, and MPEP § 609.04(a) states,

"the list may not be incorporated into the specification but must be submitted in a

separate paper." Therefore, unless the references have been cited by the examiner on

form PTO-892, they have not been considered.

Specification

7.   The disclosure is objected to because of the following informalities:

a.) The specification contains typographical errors, for example on page 32 line 35 "indtuctions" should read "instructions"

b.) The specification contains sequences which are not identified by SEQ ID No., for example on page 32 lines 11-12 and page 39 line 12. The sequences should be represented in the sequence listing and referred to by SEQ ID No. in the specification.

Appropriate correction is required for all errors throughout.

8.   The use of the trademarks RNeasy® and SMART™ RACE have been noted in this application. They should be capitalized wherever they appear and be accompanied by the generic terminology.

Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner which might adversely affect their validity as trademarks.

The trademark symbols have not been included for the trademarks. Appropriate correction is required for all trademarks throughout.

Claim Rejections - 35 USC § 112

9.   The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the

art to which it pertains, or with which it is most nearly connected, to make and use the same and shall
set forth the best mode contemplated by the inventor of carrying out his invention.

10.   Claims 43-47, 49, 50, 53, and 54 are rejected under 35 U.S.C. 112, first

paragraph, because the specification, while being enabling for a method for diagnosing

a subtype of B-cell chronic lymphocytic leukemia (B-CLL) with poor prognosis in an

individual by detecting the presence of the exon 2/exon 3 splice junction in a AMB-1

transcript, does not reasonably provide enablement for a method for diagnosing a

subtype of B-CLL with poor prognosis in an individual by detecting the presence of just

any expression product within SEQ ID No. 12-18. The specification does not enable

any person skilled in the art to which it pertains, or with which it is most nearly

connected, to make or used the invention commensurate in scope with these claims.

Factors to be considered in determining whether a disclosure meets the

enablement requirement of 35 USC 1 12, first paragraph, have been described by the

court in In re Wands, 8 USPQ2d 1400 (CA FC 1988).

> Wands states on page 1404,
> "Factors to be considered in determining whether a disclosure would require
> undue experimentation have been summarized by the board in Ex parte Forman.
> They include (1) the quantity of experimentation necessary, (2) the amount of
> direction or guidance presented, (3) the presence or absence of working
> examples, (4) the nature of the invention, (5) the state of the prior art, (6) the
> relative skill of those in the art, (7) the predictability or unpredictability of the art,
> and (8) the breadth of the claims."

The claims are broadly drawn to a method for establishing a diagnosis of a

subtype of B-cell chronic lymphocytic leukemia (B-CLL) in a individual comprising

detecting the presence or absence of at least one expression product, wherein said at

least one expression product comprises a nucleotide sequence selected from the group

consisting of SEQ ID SEQ ID No: 12, SEQ ID No: 13, SEQ ID No: 14, SEQ ID No: 15,

SEQ ID No: 16, SEQ ID No: 17 and SEQ ID No: 18 in a biological sample isolated from

the individual. A method for establishing the prognosis of a subtype of B-CLL in a

individual comprising detecting the presence or absence of at least one expression

product, wherein said at least one expression product comprises a nucleotide sequence

selected from the group consisting of SEQ ID SEQ ID No: 12, SEQ ID No: 13, SEQ ID

No: 14, SEQ ID No: 15, SEQ ID No: 16, SEQ ID No: 17 and SEQ ID No: 18 in a

biological sample isolated from the individual. A method for determining whether an

individual has a B-CLL sub-type with poor prognosis, the method comprising

determining the level of an expression product which comprises a nucleotide sequence

selected from the group consisting of SEQ ID No: 12, SEQ ID No: 13, SEQ ID No: 14,

SEQ ID No: 15, SEQ ID No: 16, SEQ ID No: 17 and SEQ ID No: 18 of said individual,

and indicating the individual as having a B-CLL sub-type with poor prognosis if the level

of the expression product is at or beyond a discriminating value and indicating the

individual as not having a B-CLL sub-type with poor prognosis if the level of the

expression product is not at or beyond the discriminating value, the discriminating value

being a value which has been determined by measuring the level of the expression

product which comprises a nucleotide sequence selected from the group consisting of

SEQ ID No: 12, SEQ ID No: 13, SEQ ID No: 14, SEQ ID No:15, SEQ ID No: 16, SEQ ID

No: 17 and SEQ ID No: 18 in both a healthy control population and a population with

known B-CLL sub-type with poor prognosis, thereby determining said discriminating

value which identifies the B-CLL sub-type population having a poor prognosis, wherein

the individual is a member of an unselected population, wherein the individual is a

member of a population

already identified as having a B-CLL sub-type with a poor prognosis, wherein the

expression product is a transcriptional product, wherein the at least one transcriptional

product is selected from the group consisting of SEQ ID No 2, SEQ ID No 4, SEQ ID No

6, SEQ ID No 7, SEQ ID No 8, SEQ ID No 9, SEQ ID No 10 and SEQ ID No 11,

wherein said at least one transcriptional product comprises a nucleotide sequence

spanning the junction between Exon-2 and Exon-3, wherein the nucleotide sequence

spanning the junction between Exon-2 and Exon-3 is the last 20 nucleotides of the 3'-

end of SEQ ID No: 15 and the first 20 nucleotides of the 5'-end of SEQ ID No: 16.

The specification discloses expression of AMB-1 in B-CLL patients without Ig VH

mutations. The specification discloses mutation of the Ig VH gene is associated with a

better prognosis in B-CLL patients. The specification discloses detection of AMB-1

transcripts by detecting the splice junction between exon 2 and exon 3 of the full length

AMB-1 transcript (SEQ ID No. 5). The specification does not disclose detection of each

of the AMB-1 transcripts in B-CLL patients with poor prognosis. The specification does

not disclose the detection of AMB-1 transcript regions other than the exon 2 and exon 3

splice junction as associated with a poor prognosis of B-CLL.

Studies identifying molecular markers to distinguish between aggressive and

non-aggressive forms of chronic lymophocytic leukemia were reviewed in Shanafelt, et

al. (Annals of Internal Medicine, 2006. Vol. 145, pages 435-447). Shanafelt, et al. teach

cytogenic abnormalities including 13q-, trisomy 12, 11q-, and 17p- with decreased

survival time for patients having 17p- and 11q- mutations. Rosenwald, et al. (Journal of

Experimental Medicine, 2001. Vol. 194, pages 1639-1647) teach a common gene

expression "signature" in CLL patients that is irrespective of Ig mutational status and

suggest combinations of genes including Ig VH and ZAP-70 as diagnostic markers for

CLL. This is contradicted by Shanafelt, et al. who teach 20-30% of patients do not have

a correlation between Ig VH mutation and ZAP-70 expression and 30-40% of patients

do not have a correlation between CD38 expression and mutation status.

There is insufficient evidence or nexus that would lead the skilled artisan to

predict the ability to diagnose a poor prognosis of B-CLL by detecting just any AMB-1

transcript. The specification does not teach detection of transcript regions associated

with B-CLL prognosis other than the exon 2 and exon 3 splice junction. Additionally,

alignment of the sequences in SEQ ID Nos. 12-18 with SEQ ID No. 11 did not produce

a consensus sequence in SEQ ID No. 11 that is common with SEQ ID Nos. 12-18 (see

sequence alignment). Therefore, detection of even a portion of SEQ ID No. 11 would

not necessarily detect SEQ ID Nos. 12-18 and detection of a region other than the

splice junction between exon 2 and exon 3 in SEQ ID No. 11 would not be predictive of

a poor prognosis in B-CLL patients.

In view of the lack of the predictability of the art to which the invention pertains

undue experimentation would be required to practice the claimed methods in a

reasonable expectation of success, absent a specific and detailed description in

applicant's specification of how to effectively practice the claimed methods and absent

working examples providing evidence which is reasonably predictive that the claimed

methods are effective for determining a poor prognosis of B-CLL commensurate in

scope with the claimed invention.

Conclusion

11.   No claims are allowed.

12.   Claims 43-47, 49, 50, 53, and 54 are free of the prior art. The closest prior art is

Oscier, et al. (Blood, 2002. Vol. 100, pages 1177-1184, as cited on the IDS).

Oscier, et al. teach a method of determining the prognosis of B-CLL in patients

by detecting a mutation in the IGVH gene. Oscier, et al. do not teach nor reasonably

suggest determining a poor prognosis of B-CLL patients by detecting the sequence of

SEQ ID No. 11.

13.   Any inquiry concerning this communication or earlier communications from the

examiner should be directed to Anne M. Gussow whose telephone number is (571) 272-

6047. The examiner can normally be reached on Monday - Friday 8:30 am - 5 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's

supervisor, Larry Helms can be reached on (571) 272-0832. The fax phone number for

the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the

Patent Application Information Retrieval (PAIR) system. Status information for

published applications may be obtained from either Private PAIR or Public PAIR.

Status information for unpublished applications is available through Private PAIR only.

For more information about the PAIR system, see http://pair-direct.uspto.gov. Should

you have questions on access to the Private PAIR system, contact the Electronic

Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a

USPTO Customer Service Representative or access to the automated information

system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Anne M. Gussow

November 7, 2007

LARRY R. HELMS, PH.D.
SUPERVISORY PATENT EXAMINER

10535500-11_vs_10535500allna.txt

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OM nucleic - nucleic search, using sw model

Run on: October 30, 2007, 14:45:28 ; Search time 159 seconds
(without alignments)
17.371 Million cell updates/sec

Title: us-10-535-500a-11
Perfect score: 9458
Sequence: 1 atttgaattggtgaacttag.........aatttatcaataaatgccag 9458

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 0.5

Searched: 42 seqs, 146011 residues

Total number of hits satisfying chosen parameters: 84

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : US10535500A.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	DB Length	DB	ID	Description
1	9458	100.0	9458	1	US-10-535-500A-11	sequence 11, Appl
2	9458	100.0	19999	1	US-10-535-500A-1	sequence 1, Appl
3	9458	100.0	89650	1	US-10-535-500A-4	sequence 5, Appl
4	4649.5	49.2	6209	1	US-10-535-500A-4	sequence 4, Appl
5	2333.5	24.7	3893	1	US-10-535-500A-7	sequence 2, Appl
6	1956	20.7	2817	1	US-10-535-500A-10	sequence 7, Appl
7	1955	20.7	1955	1	US-10-535-500A-16	sequence 10, Appl
8	1955	20.7	1955	1	US-10-535-500A-6	sequence 16, Appl
9	1955	20.7	2260	1	US-10-535-500A-15	sequence 6, Appl
10	557	5.9	557	1	US-10-535-500A-18	sequence 15, Appl
11	366	3.9	366	1	US-10-535-500A-14	sequence 18, Appl
12	307	3.2	307	1	US-10-535-500A-8	sequence 14, Appl
13	307	3.2	1970	1	US-10-535-500A-13	sequence 8, Appl
14	305	3.2	305	1	US-10-535-500A-5	sequence 13, Appl
15	207.8	2.2	89650	1	US-10-535-500A-5	sequence 5, Appl
16	142.7	1.5	19999	1	US-10-535-500A-1	sequence 1, Appl
17	50.8	0.5	1970	1	US-10-535-500A-8	sequence 8, Appl
18	50.8	0.5	1989	1	US-10-535-500A-9	sequence 9, Appl
19	44.1	0.5	6209	1	US-10-535-500A-4	sequence 4, Appl
20	44.1	0.5	9458	1	US-10-535-500A-11	sequence 11, Appl
21	34	0.4	1955	1	US-10-535-500A-10	sequence 10, Appl
22	34	0.4	1955	1	US-10-535-500A-16	sequence 16, Appl
23	34	0.4	2260	1	US-10-535-500A-6	sequence 6, Appl

Page 1

24	34	0.4	2817	1	US-10-535-500A-7	sequence 7, Appl
25	34	0.4	3893	1	US-10-535-500A-2	sequence 2, Appl
26	29.4	0.3	366	1	US-10-535-500A-18	sequence 18, Appl
27	25.2	0.3	1989	1	US-10-535-500A-9	sequence 9, Appl
28	25	0.3	25	1	US-10-535-500A-43	sequence 43, Appl
29	24.2	0.2	557	1	US-10-535-500A-15	sequence 15, Appl
30	23.2	0.2	1253	1	US-10-535-500A-17	sequence 17, Appl
31	22	0.2	22	1	US-10-535-500A-32	sequence 32, Appl
32	21.2	0.2	305	1	US-10-535-500A-13	sequence 13, Appl
33	21.2	0.2	307	1	US-10-535-500A-14	sequence 14, Appl
34	21	0.2	21	1	US-10-535-500A-19	sequence 19, Appl
35	21	0.2	21	1	US-10-535-500A-20	sequence 20, Appl
36	21	0.2	21	1	US-10-535-500A-21	sequence 21, Appl
37	21	0.2	21	1	US-10-535-500A-22	sequence 22, Appl
38	21	0.2	21	1	US-10-535-500A-23	sequence 23, Appl
39	21	0.2	21	1	US-10-535-500A-25	sequence 25, Appl
40	21	0.2	21	1	US-10-535-500A-26	sequence 26, Appl
41	21	0.2	21	1	US-10-535-500A-30	sequence 30, Appl
42	21	0.2	21	1	US-10-535-500A-31	sequence 31, Appl
43	20.6	0.2	1253	1	US-10-535-500A-17	sequence 17, Appl
44	20	0.2	20	1	US-10-535-500A-41	sequence 41, Appl
45	20	0.2	20	1	US-10-535-500A-42	sequence 42, Appl

ALIGNMENTS

RESULT 1
US-10-535-500A-11
; Sequence 11, Application US/10535500A
; GENERAL INFORMATION:
; APPLICANT: Rigshospitalet
; APPLICANT: Henrik Leffers
; APPLICANT: Anne Mette Buhl Hertz
; APPLICANT: Jorgen Kjems
; TITLE OF INVENTION: Methods and kits for diagnosing and
; TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
; FILE REFERENCE: P34546US01
; CURRENT APPLICATION NUMBER: US/10/535,500A
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: DK/PA 200201792
; PRIOR FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-535-500A-11

Query Match 100.0%; Score 9458; DB 1; Length 9458;
Best Local Similarity 100.0%; Pred. No. 3.3e-86;
Matches 9458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ATTTGAATTGGTGAAAGCTTAGTAAAGCAGCGGCCTCCACCAATAAGGCAGGCATCATCC 60
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Db   1 ATTTGAATTGGTGAAAGCTTAGTAAAGCAGCGGCCTCCACCAATAAGGCAGGCATCATCC 60

Qy   61 AATCTGTCGAAAGCTTGAATAAAACAAAAAGAGGAAGGAAAATTTGCTTCTTTTCTTCT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATCTGTCGAAAGCTTGAATAAAACAAAAAGAGGAAGGAAAATTTGCTTCTTTTCTTCT 120

Qy 121 TGATCTAGTAGTATCATCTTCTCCGCCTTGGATGTGAGTGGGCTTCAGACTTAAACCA 180

Page 2

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1081 Qy  ACTAGGCTGCACTGTCTGTAGAGAATCTGAAAAAAATAATAGAGTCACTGAAATGCAGTT 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1081 Db  ACTAGGCTGCACTGTCTGTAGAGAATCTGAAAAAAATAATAGAGTCACTGAAATGCAGTT 1140

1141 Qy  GGTATAATTATTGCCATGCATCATATATCTAAATCACTAGTGGTCAAATACTCTTCCC 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1141 Db  GGTATAATTATTGCCATGCATCATATATCTAAATCACTAGTGGTCAAATACTCTTCCC 1200

1201 Qy  TGAAAAACATTTTCTTGGTTGAATTCTAAATAATTGTTGGTCACCACTGAGCTTT 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
1201 Db  TGAAAAACATTTTCTTGGTTGAATTCTAAATAATTGTTGGTCACCACTGAGCTTT 1260

1261 Qy  AAATATAAAATACTTTCAAGTTTGCATATTTTATTACCTGTTCCTTAACAAACATTGA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 Db  AAATATATAAATACTTTCAAGTTTGCATATTTTATTACCTGTTCCTTAACAAACATTGA 1320

1321 Qy  ATTCAACATGAAAATGATTATGGGAAACATTCGGGTATACAGTCCCTGACTCTTAAGGAC 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1321 Db  ATTCAACATGAAAATGATTATGGGAAACATTCGGGTATACAGTCCCTGACTCTTAAGGAC 1380

1381 Qy  TCAGGTAAATACTTAGGGTATTTCATGGCCCTAGTCTTTGGGGTACCCACATGTTCTTCT 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1381 Db  TCAGGTAAATACTTAGGGTATTTCATGGCCCTAGTCTTTGGGGTACCCACATGTTCTTCT 1440

1441 Qy  TCAAATCACAGATTCAAAATCAAGATGATAACACAGTGATTGTGTAGACAAAATAAGTG 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1441 Db  TCAAATCACAGATTCAAAATCAAGATGATAACACAGTGATTGTGTAGACAAAATAAGTG 1500

1501 Qy  AACCAAAATTGCTTGCTTCTGTCATTCTATGGAACCACTGAGAGTTTTTACTTGTGCTTA 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1501 Db  AACCAAAATTGCTTGCTTCTGTCATTCTATGGAACCACTGAGAGTTTTTACTTGTGCTTA 1560

1561 Qy  AAATTTTGAATAGTAAAACAGAGTGTCAACTTCATGCTGGAATATTTTGGCTTTTAGA 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1561 Db  AAATTTTGAATAGTAAAACAGAGTGTCAACTTCATGCTGGAATATTTTGGCTTTTAGA 1620

1621 Qy  CACAATTTTAAGTACATGAAGTATTTTACAGACTAAGTAACATCACTGAAATTACAGC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1621 Db  CACAATTTTAAGTACATGAAGTATTTTACAGACTAAGTAACATCACTGAAATTACAGC 1680

1681 Qy  TTTCTTCTTTTAAAACTGGTATTTGTTATAAAACTAAAGAGCGAATCAAGAAAAGCATA 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1681 Db  TTTCTTCTTTTAAAACTGGTATTTGTTATAAAACTAAAGAGCGAATCAAGAAAAGCATA 1740

1741 Qy  ATTATTACTGATTATTACAGGATTATTACTGAAAAAGAAATGTACGGAATAGAGGAGGAA 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1741 Db  ATTATTACTGATTATTACAGGATTATTACTGAAAAAGAAATGTACGGAATAGAGGAGGAA 1800

1801 Qy  GGAGTAACAAATGACCTCCTCTGGGTGTTGAAAACACCAATAAGCCTGCTTCCAGGAAG 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1801 Db  GGAGTAACAAATGACCTCCTCTGGGTGTTGAAAACACCAATAAGCCTGCTTCCAGGAAG 1860

1861 Qy  TGCCTAAGACAGAGCTGGCTCAGCTTGCTGGGTCACAGCATGTAAGGAAACTGCTGGGCT 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1861 Db  TGCCTAAGACAGAGCTGGCTCAGCTTGCTGGGTCACAGCATGTAAGGAAACTGCTGGGCT 1920

1921 Qy  ACATGCCACCATCCTCAGTTGTCCAGATAGATAATCCCATAGCCCCATGGGGAAATAATC 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1921 Db  ACATGCCACCATCCTCAGTTGTCCAGATAGATAATCCCATAGCCCCATGGGGAAATAATC 1980

1981 Qy  TTTAATTTATGATATAGTGACACCATTCAAAGCACTATGCTAAGTCCTTTATGTGAATTA 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1981 Db  TTTAATTTATGATATAGTGACACCATTCAAAGCACTATGCTAAGTCCTTTATGTGAATTA 2040
```

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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 121 Qy  TGATCTAGTATATCATCTTCTCCTGCCCTTGGATGTGAGTGGGCCTTCAGACTTAAACCA 180

 181 Qy  GGAGTTACACCTTGGCTTCCCTGGTTCTCAGTTCTTGGACTTGGACTTACACTG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 181 Db  GGAGTTACACCTTGGCTTCCCTGGTTCTCAGTTCTTGGACTTGGACTTACACTG 240

 241 Qy  CCAGGTTCCTGGTTCTCCAGCTTGCGAGATGGCAGATCATGGGACTTCTTGGCCTCCATA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 241 Db  CCAGGTTCCTGGTTCTCCAGCTTGCAGATGGCAGATCATGGGACTTCTTGGCCTCCATA 300

 301 Qy  ATTGTGTGAGTCAATTCATTTATTACATATCCAGTTATGCATTGCTTAACAATGGA 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 301 Db  ATTGTGTGAGTCAATTCATTTATTACATATCCAGTTATGCATTGCTTAACAATGGA 360

 361 Qy  GACAGGTTCTGAGAAATGCATTGTAAGTGATTTCATCATTGTGCAAACATCATAGAGTG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 361 Db  GACAGGTTCTGAGAAATGCATTGTAAGTGATTTCATCATTGTGCAAACATCATAGAGTG 420

 421 Qy  TAACTACACAAACCTGGACAGCATAGACTACTACACATCTAGGCTACGTGTAGCTTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 421 Db  TAACTACACAAACCTGGACAGCATAGACTACTACACATCTAGGCTACGTGTAGCTTG 480

 481 Qy  TAACCTCATGATAAGTATAAACATCATGATAAGTATGTATGTATCTACCATATCTAA 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 481 Db  TAACCTCATGATAAGTATAAACATCATGATAAGTATGTATGTATCTACCATATCTAA 540

 541 Qy  ATGTAGAAAAGGTACAGTAAAAATATGGTATAATCTTATGGGATCACCATCATATATGCA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 541 Db  ATGTAGAAAAGGTACAGTAAAAATATGGTATAATCTTATGGGATCACCATCATATATGCA 600

 601 Qy  ATCCTTGTAGACTGAAATGTCATTGTGTAGTGCATGTATACGCACACATACACAA 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 601 Db  ATCCTTGTAGACTGAAATGTCATTGTGTAGTGCATGTATACGCACACATACACAA 660

 661 Qy  ACACACACAAATATACTATTGGTTCTTTTCTCTGAAGAGCCCTAATACAATATGTTATA 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 661 Db  ACACACACAAATATACTATTGGTTCTTTTCTCTGAAGAGCCCTAATACAATATGTTATA 720

 721 Qy  CATTTATTATTGACTCTATTTCAAAATTTATGGTTTGGTGAAACATATGTGGAGATGGGG 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 721 Db  CATTTATTATTGACTCTATTTCAAAATTTATGGTTTGGTGAAACATATGTGGAGATGGGG 780

 781 Qy  CATAGGTGTGTGAACTGGGATAGTGTCCTGCTGATGAATGGGTGGGAGGCATCATTTGGG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 781 Db  CATAGGTGTGTGAACTGGGATAGTGTCCTGCTGATGAATGGGTGGGAGGCATCATTTGGG 840

 841 Qy  ACAAGCCCAGGGCATCAGCTTATAGATCAAGAGCTCAACAAGAGCACTTTATGGCAAA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 841 Db  ACAAGCCCAGGGCATCAGCTTATAGATCAAGAGCTCAACAAGAGCACTTTATGGCAAA 900

 901 Qy  ACCTCCCACAAGACCTCCAGAAGTTGAGAAACTGCTAAAAGTTTCTTTATGACAGATGA 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 901 Db  ACCTCCCACAAGACCTCCAGAAGTTGAGAAACTGCTAAAAGTTTCTTTATGACAGATGA 960

 961 Qy  CATTTATGGATAAAATAGGGATTAGCAGGATTCTTAAATACTTCGAACACTAACCTTC 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 961 Db  CATTTATGGATAAAATAGGGATTAGCAGGATTCTTAAATACTTCGAACACTAACCTTC 1020

1021 Qy  ATTTCTACCAGGCAGTGGGGCCCCAAGTGCAGGGCCCATAGGGAAGTACAAGTCTCGGGAAGAT 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1021 Db  ATTTCTACCAGGCAGTGGGGCCCCAAGTGCAGGGCCCATAGGGAAGTACAAGTCTCGGGAGAT 1080
```

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Qy  2041  ACTTTTGTCAAATTTATTTTCATAAATAACCCAAATATGTATACCACTATTATCCTACC  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  ACTTTTGTCAAATTTATTTTCATAAATAACCCAAATATGTATACCACTATTATCCTACC  2100

Qy  2101  TTAAAGAGGAGAAACTGAGCTCCTAAAGTTAAATATCTAACCCAAGTTAAGACTGCTAG  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  TTAAAGAGGAGAAACTGAGCTCCTAAAGTTAAATATCTAACCCAAGTTAAGACTGCTAG  2160

Qy  2161  TCACCCTAGGCTATTAACTCAGGCAGTCTAACTCAGGTATAATAACATTATGCTACTGTT  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  TCACCCTAGGCTATTAACTCAGGCAGTCTAACTCAGGTATAATAACATTATGCTACTGTT  2220

Qy  2221  TGCAGCTTTGACTATGCCTGAATTATAACGTCATGCTATCTAACTAAAAAGCTAAGGGAA  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  TGCAGCTTTGACTATGCCTGAATTATAACGTCATGCTATCTAACTAAAAAGCTAAGGGAA  2280

Qy  2281  ATAAAATGAGCCATAGGGCTCAATTCATAAAAGGAGAGAAAATACTGGGGAAAAGTGAT  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  ATAAAATGAGCCATAGGGCTCAATTCATAAAAGGAGAGAAAATACTGGGGAAAAGTGAT  2340

Qy  2341  AATGCAGAGTTTAAAATATTTTGTAAAAGTGCCAGAGATTGAGTATAACAAGTGTGACC  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  AATGCAGAGTTTAAAATATTTTGTAAAAGTGCCAGAGATTGAGTATAACAAGTGTGACC  2400

Qy  2401  AAAAAAAAAAAAAAAAAAAAAAAAGGAAGAAGGTAAAAAAAGAGGGAGGTCTGAGAAAT  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  AAAAAAAAAAAAAAAAAAAAAAAAGGAAGAAGGTAAAAAAAGAGGGAGGTCTGAGAAAT  2460

Qy  2461  AGAAATATCAGAGGAGGGAAGGGAAATAAAGGAGGGTGAGAGTAAATTCTCTTTAGCATTCAGA  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  AGAAATATCAGAGGAGGGAAGGGAAATAAAGGAGGGTGAGAGTAAATTCTCTTTAGCATTCAGA  2520

Qy  2521  TTCCACAGATTCCACAAATCACATTTCTTTTTACCAACTAAGGAAAAATAACACTTGA  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  TTCCACAGATTCCACAAATCACATTTCTTTTTACCAACTAAGGAAAAATAACACTTGA  2580

Qy  2581  CCTAACATTTCATTGGAGTTAGCTAAAGGATGCTAGAAAAACTATGTTGCAGTGGTTTGC  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  CCTAACATTTCATTGGAGTTAGCTAAAGGATGCTAGAAAAACTATGTTGCAGTGGTTTGC  2640

Qy  2641  TCTAATTTCTTCAGGAAATACAGAATTGGAGTAGGAATAGAGAAAGATCAGAGAAAGGAA  2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  TCTAATTTCTTCAGGAAATACAGAATTGGAGTAGGAATAGAGAAAGATCAGAGAAAGGAA  2700

Qy  2701  CTATCAGAAAAATACAGAATTGGAGTAGGATATAACATATTTGGGTTGAAGGTAAAATT  2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CTATCAGAAAAATACAGAATTGGAGTAGGATATAACATATTTGGGTTGAAGGTAAAATT  2760

Qy  2761  TATATTGTAATCTTAAGTATCTTGCTACTTCAGTTGGTCCCTGGAACAGCAGCAGTCAGA  2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TATATTGTAATCTTAAGTATCTTGCTACTTCAGTTGGTCCCTGGAACAGCAGCAGTCAGA  2820

Qy  2821  ATCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGGTCCCAGACTCACTGGAATC  2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  ATCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGGTCCCAGACTCACTGGAATC  2880

Qy  2881  AGAATATAAAATACTGACAAGATGCCCCGGGATTCATATGCAGTAGAGCTGGCGAAGTT  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  AGAATATAAAATACTGACAAGATGCCCCGGGATTCATATGCAGTAGAGCTGGCGAAGTT  2940

Qy  2941  CCATTGTAGCCTGTGATTGTTTCTGCAACTTAGTATTTCTGAGTTTCCCAAGGAAGAA  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db  2941  CCATTGTAGCCTGTGATTGTTTCTGCAACTTAGTATTTCTGAGTTTCCCAAGGAAGAA  3000

Qy  3001  AACCCAGGCCCTTAGCTTCTGGCAGACTTGTGTTCTCCTTACTACTAGCTGCATGACT  3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  AACCCAGGCCCTTAGCTTCTGGCAGACTTGTGTTCTCCTTACTACTAGCTGCATGACT  3060

Qy  3061  CATGAGCAAGGAAATCAAACTTTATGTGCCTGAGTTCCTCATCTATAAAAATGGAGACTA  3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CATGAGCAAGGAAATCAAACTTTATGTGCCTGAGTTCCTCATCTATAAAAATGGAGACTA  3120

Qy  3121  TAATAATCATCTCCTAGGCTGTTTGAGGATGTCAACAAATGCTCCTTTCATTCCTCT  3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  TAATAATCATCTCCTAGGCTGTTTGAGGATGTCAACAAATGCTCCTTTCATTCCTCT  3180

Qy  3181  ATTTACAGACCTGCCGCAGCAATTCTGTGGACTAACCTCTGAAATAAATAAGCTGATTATTTAT  3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  ATTTACAGACCTGCCGCAGCAATTCTGTGGACTAACCTCTGAAATAAATAAGCTGATTATTTA  3240

Qy  3241  AACTTAGTAATTGAGTGTGATCTGGACTAACCTCTGAAATAAATAAGCTGATTATTTAC  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  AACTTAGTAATTGAGTGTGATCTGGACTAACCTCTGAAATAAATAAGCTGATTATTTAC  3300

Qy  3301  TTATTTCTCAAAACAACACAGAATACGATTTAGCAAATACTTCTTAAGATATATTTTAC  3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  TTATTTCTCAAAACAACACAGAATACGATTTAGCAAATACTTCTTAAGATATATTTTAC  3360

Qy  3361  ATTTCTATATTCTCCTACCCTGAGTTGATGTGTGAGCAATATGTCACTTCATAAAGCCA  3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  ATTTCTATATTCTCCTACCCTGAGTTGATGTGTGAGCAATATGTCACTTCATAAAGCCA  3420

Qy  3421  GGTATACATTATGGACAGTAAGTAAGTAAAAACATATTATTCTACGTTTTGTCCAAA  3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  GGTATACATTATGGACAGTAAGTAAGTAAAAACATATTATTCTACGTTTTGTCCAAA  3480

Qy  3481  AATTTAAATTTCAACTGTTGCCGTGTGTTGGTAATGTAAAAACAAACTCAGTACACGTAG  3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  AATTTAAATTTCAACTGTTGCCGTGTGTTGGTAATGTAAAAACAAACTCAGTACACGTAG  3540

Qy  3541  TATTCAGTACAGTATTTAAGCCCCTGTACTTAAACATATTCCTCGTACCAATGAAGTTAC  3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  TATTCAGTACAGTATTTAAGCCCCTGTACTTAAACATATTCCTCGTACCAATGAAGTTAC  3600

Qy  3601  ATGAAAGCAAATTTGTGTGAGATATCGTAGATGGAAGTAAATAGTCTTTATGTTCCCC  3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  ATGAAAGCAAATTTGTGTGAGATATCGTAGATGGAAGTAAATAGTCTTTATGTTCCCC  3660

Qy  3661  ACAAATTGAAATGCATTCAAAAACTCTGTGTGCTTGGTTGCCTCCATAAGTGGCTATGATTAA  3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  ACAAATTGAAATGCATTCAAAAACTCTGTGTGCTTGGTTGCCTCCATAAGTGGCTATGATTAA  3720

Qy  3721  GTGAGAGAGACAGCAGAGAGATACGCTTGGTGCCTCCATAAGTGGCTATGATTAA  3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  GTGAGAGAGACAGCAGAGAGATACGCTTGGTGCCTCCATAAGTGGCTATGATTAA  3780

Qy  3781  TAAGACCAAGTTTTCTAAAGAAAATGAGATCATAACAAAAGCCCTCTTATGACTATCTT  3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  TAAGACCAAGTTTTCTAAAGAAAATGAGATCATAACAAAAGCCCTCTTATGACTATCTT  3840

Qy  3841  TTATCAGGGGCAAAAAGGAAAGACACAAAACAGCATGAAATGATGAGACCAAGTGATGAA  3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  TTATCAGGGGCAAAAAGGAAAGACACAAAACAGCATGAAATGATGAGACCAAGTGATGAA  3900

Qy  3901  AATTCATTCACAATGATTGCTTCAAGAGTAATTTCTCTTGGGTAATTCAGCAGCCTGTT  3960

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Qy 4861 TCAACAGCTATTCCCACCCCTCGATGAAATATCACCCAGTCAATTGTTTTCCTAGT 4920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4861 TCAACAGCTATTCCCACCCCTCGATGAAATATCACCCAGTCAATTGTTTTCCTAGT 4920

Qy 4921 TTGGGTAATGGCCCTCTGGGCAGGACTGGAGTGGGCACACAGGAGGAAGCTGCAAACTAT 4980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4921 TTGGGTAATGGCCCTCTGGGCAGGACTGGAGTGGGCACACAGGAGGAAGCTGCAAACTAT 4980

Qy 4981 GTTTAGAAGCATGTCTGGGAAATGTCATGCAAGAAAAGACATATTTAAAGGTAGGCTTTG 5040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4981 GTTTAGAAGCATGTCTGGGAAATGTCATGCAAGAAAAGACATATTTAAAGGTAGGCTTTG 5040

Qy 5041 CATGAATGGAAAAGGAGGAGTAATTCTATGTAGAGCAGAGCCTCTTACTTGCAGTGACAGA 5100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5041 CATGAATGGAAAAGGAGGAGTAATTCTATGTAGAGCAGAGCCTCTTACTTGCAGTGACAGA 5100

Qy 5101 AGCAAAAGTGGGGAAGCAAGAGGAATTATGCTTTCATCAGCCAAATTTGCAGGTAGGGAG 5160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5101 AGCAAAAGTGGGGAAGCAAGAGGAATTATGCTTTCATCAGCCAAATTTGCAGGTAGGGAG 5160

Qy 5161 GATTGGCTCAGTCATCTTGGCTGAGGCTCATGAAACCAGTGTAAAGAAAGTGGACTAGA 5220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5161 GATTGGCTCAGTCATCTTGGCTGAGGCTCATGAAACCAGTGTAAAGAAAGTGGACTAGA 5220

Qy 5221 TTAATTTCATCCATTACAGGAAGAGGAGCCGTGAAAGATAATCCAGAAATCATTGGGATT 5280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5221 TTAATTTCATCCATTACAGGAAGAGGAGCCGTGAAAGATAATCCAGAAATCATTGGGATT 5280

Qy 5281 TGATGGTAGAAGGTATTTGGGACTATTCCATTTGAAATGAGAAGGTACCTGACATTCTT 5340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5281 TGATGGTAGAAGGTATTTGGGACTATTCCATTTGAAATGAGAAGGTACCTGACATTCTT 5340

Qy 5341 TGAATTCCTTCAAGCAAAGGATTAAATTACCCATGAGTTGACTCAGAAAAAACATAAA 5400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5341 TGAATTCCTTCAAGCAAAGGATTAAATTACCCATGAGTTGACTCAGAAAAAACATAAA 5400

Qy 5401 AAGTATTGTTGCTCTGCTCAGAGTTTATCTAACTCATTCTCACTTCTTATTCCATGATG 5460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5401 AAGTATTGTTGCTCTGCTCAGAGTTTATCTAACTCATTCTCACTTCTTATTCCATGATG 5460

Qy 5461 AAATGACATAAATGAGGTTTTATTGTTTGTTGTTGTTTCTGGACACAAGGCAAGG 5520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5461 AAATGACATAAATGAGGTTTTATTGTTTGTTGTTGTTTCTGGACACAAGGCAAGG 5520

Qy 5521 TAGCTACCTGGGCAGAGCTGTTTATTTCTCTATGCCGTGGAGAGAAATTGGTTAATTGG 5580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5521 TAGCTACCTGGGCAGAGCTGTTTATTTCTCTATGCCGTGGAGAGAAATTGGTTAATTGG 5580

Qy 5581 CCATGGAAGGCAGTCATTAAGATGTTCCCATGCGAGTGAACTTTCCAGGGTTCCCAGCTT 5640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5581 CCATGGAAGGCAGTCATTAAGATGTTCCCATGCGAGTGAACTTTCCAGGGTTCCCAGCTT 5640

Qy 5641 CTGCATCCTTCCCTGTCCCTCAATTCCATTGTTGGTGATGACAATGTCTCTCCCATCAGC 5700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5641 CTGCATCCTTCCCTGTCCCTCAATTCCATTGTTGGTGATGACAATGTCTCTCCCATCAGC 5700

Qy 5701 CTCATGAAGTTCTCTCCATTTATTAAAATTTGCTTTCAGGAAAAATTTGAAAATGTGT 5760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5701 CTCATGAAGTTCTCTCCATTTATTAAAATTTGCTTTCAGGAAAAATTTGAAAATGTGT 5760

Qy 5761 CCAGTAATGCCTGATTGGCCCCTTATCCTAAAGGCTAAACTGGAGGAAGGAAGCTAAAC 5820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5761 CCAGTAATGCCTGATTGGCCCCTTATCCTAAAGGCTAAACTGGAGGAAGGAAGCTAAAC 5820

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Db 3901 AATTCATTCACAATGATTGCTTCAAGAGTAATTTCTCCTGGGTAATTCAGCAGCCTGTT 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy

Qy 3961 ACTATGGCTCTCTGGAGTGATAGCTAATGTAAATGAAGCCTCTAAAAGTGGATTATCCTG 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3961 ACTATGGCTCTCTGGAGTGATAGCTAATGTAAATGAAGCCTCTAAAAGTGGATTATCCTG 4020

Qy 4021 ACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATT 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4021 ACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAAATT 4080

Qy 4081 CAAAAGAATAAAATATTCTTTTAAAGTTAATGACCTACGATCCATTTCTTCC 4140
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4081 CAAAAGAATAAAATATTCTTTTAAAGTTAATGACCTACGATCCATTTCTTCC 4140

Qy 4141 CTGACTAACAAGCAGCAAGCACTTAAAAATATCCAGCCAGGATGAAATAGAAACCCACCT 4200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4141 CTGACTAACAAGCAGCAAGCACTTAAAAATATCCAGCCAGGATGAAATAGAAACCCACCT 4200

Qy 4201 GACTTGTAATATTTTTGTTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTTGAAT 4260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4201 GACTTGTAATATTTTTGTTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTTGAAT 4260

Qy 4261 GATCTTGGCAAATGTCTCGAATTATTTTCTTTATCTTGGAAAAAAGTT 4320
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 4261 GATCTTGGCAAATGTCTCGAATTATTTTCTTTATCTTGGAAAAAAGTT 4320

Qy 4321 TCATGAATGGGGTGTCAAAATTGATTAGTTTAAAAACCTTTCTGCAGATACGTATGGCA 4380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4321 TCATGAATGGGGTGTCAAAATTGATTAGTTTAAAAACCTTTCTGCAGATACGTATGGCA 4380

Qy 4381 CCCTAAAACTGTATTAGAAAAAAAGTAAGTACTCTGTAGTGTGAAAATTCTTAAAGGAC 4440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4381 CCCTAAAACTGTATTAGAAAAAAAGTAAGTACTCTGTAGTGTGAAAATTCTTAAAGGAC 4440

Qy 4441 ACCCTCTTTACAAAACTCACAAAAAACAGCCTTGGAATACCCACATGAAGTAGCTGTTGT 4500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4441 ACCCTCTTTACAAACTCACAAAAAACAGCCTTGGAATACCCACATGAAGTAGCTGTTGT 4500

Qy 4501 TATTGCTTCTATATACCTACACTCTGTCTATTATAAAAAGACTGGTTTTTGGCAGGTGT 4560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4501 TATTGCTTCTATATACCTACACTCTGTCTATTATAAAAAGACTGGTTTTTGGCAGGTGT 4560

Qy 4561 GGTGGCTCACACCTGTAATTCCAGCACTTTGGGAGGCCGAAGGCGGGCCGGATCACCTGAGA 4620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4561 GGTGGCTCACACCTGTAATTCCAGCACTTTGGGAGGCCGAAGGCGGGCCGGATCACCTGAGA 4620

Qy 4621 TCAGGAGTTCAGGACCAGCCTGATCAATATGGTGAAACCCAGTCTTTACTGAAAATACAA 4680
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Db 4621 TCAGGAGTTCAGGACCAGCCTGATCAATATGGTGAAACCCAGTCTTTACTGAAAATACAA 4680

Qy 4681 AAATCACCCGGGTGTGGTGACAGGGCCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAG 4740
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Db 4681 AAATCACCCGGGTGTGGTGACAGGGCCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAG 4740

Qy 4741 GAGAATCACTTGAACCTCAGGAGGTCAGAGGTTGCAGTGAGCTGAGATCATGCCCACTGCACT 4800
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Db 4741 GAGAATCACTTGAACCTCAGGAGGTCAGAGGTTGCAGTGAGCTGAGATCATGCCCACTGCACT 4800

Qy 4801 CCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAAGACTGTTTT 4860
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Db 4801 CCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAAGACTGTTTT 4860

Qy 5821 TGAGAAATCTTGCAAATGCTGAGCCAAAAACGTATTAATAGCAAGATCTATCATTTATT 5880
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Db 5821 TGAGAAATCTTGCAAATCATTGAGCCAAAAACGTATTAATAGCAAGATCTATCATTTATT 5880

Qy 5881 GACTAGTATGTGGCAGGCAGTGCCCTTTATTTAGGCAGGGAGAGTTGATGGGGGGGGCG 5940
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Db 5881 GACTAGTATGTGGCAGGCAGTGCCCTTTATTTAGGCAGGGAGAGTTGATGGGGGGGGCG 5940

Qy 5941 GGGTCACACATCTTAAAGAGGTGCTATCCTCCTATATAAATCATGTAAGTCAAGAGA 6000
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Db 5941 GGGTCACACATCTTAAAGAGGTGCTATCCTCCTATATAAATCATGTAAGTCAAGAGA 6000

Qy 6001 GTAAGGAATTGTCTTCTTGTTTGGTTATATTCAGGGGATTAGAGTATACAGTAGAAGATCCC 6060
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Qy 6061 AAGAAACCTTGGGGATCATTTAGACTAAGAAATGCCAATACCGCCGGGCGCGGTGGCTCA 6120
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Qy 6121 CGCCTGTAATCCCAGCACTTGAGAGGCCGAGGTGGGCGGATCACAAGGTCAGGAGATTG 6180
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Db 6121 CGCCTGTAATCCCAGCACTTGAGAGGCCGAGGTGGGCGGATCACAAGGTCAGGAGATTG 6180

Qy 6181 AGACCGCTCCTGGCTAACGTGGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTAGCCG 6240
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Qy 6241 GGCGTGGTGGCGGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGTG 6300
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Qy 6301 TGAACTCAGGAGGCGGAGCTTGCAGTCAGCCGAGATTGCCCCAATGCACTCCAGCCTGGG 6360
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Qy 6421 AGAGCCAAATCATGAACATCATGAAGGGTAGCTAAACAAATGTTGGCAGTGAGCCTAGTGGTTAAGAG 6480
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Db 6421 AGAGCCAAATCATGAACATCATGAAGGGTAGCTAAACAAATGTTGGCAGTGAGCCTAGTGGTTAAGAG 6480

Qy 6481 AGCAGACTCTTAACTAGAACACTGCACTCCACTGTCCTCACTGTAGACCCTCACTGTGGGG 6540
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Qy 6541 TTCTAATTAACCCCTGTTACTTACCAGTGGCAGTCTTAAGGCATTCCTTAAGTTCGTTGT 6600
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Qy 6661 ACTGTGAGCGATTAAATGAGTTACTACTGTATTTGTAAAGTGCTTAAAATGCTGTCTCCAAA 6720
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Qy 6721 AGAGTTTGTTAAACACTTAAGAACTGATTTACTTACTGAGCATCTAAACTGACAGCTCTCAATAA 6780
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Db 6721 AGAGTTTGTTAAACACTTAAGAACTGATTTACTTACTGAGCATCTAAACTGACAGCTCTCAATAA 6780

Qy 6781 CTGGAAATGATCAAGCATAGGCCCTGGAATATAAGCAGGTCTACATGAAGGCAAAAATGT 6840
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Qy 6841 TCGTTCTTTTGTTCAGCCGTGTGCCTAGATCAATATCTAGTGATCATGTGCTCAAGAAATA 6900
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Qy 6901 TTGTTGAATGAATCAATGAACCTACCGGAGTAGTTACATAAAAGAGTTCTGCATGAGTAC 6960
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Qy 7021 GGAACTGATAAATTGGTGTATACAATGTAAAAAAATGTGCCTATATGATTTGAGAAAAA 7080
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Qy 7081 CTTATTTCTCTCCCTTTTCTTCCTTCTTCCTTCCTTCTTCTTCCTTCTTCCTTCTTCCTCC 7140
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Qy 7201 TCTTCTTCTTCTTCCTTCTTCTTCCTTCTTCTTCTGTCTGTCCTTCCTTCTTTCCTTCCTT 7260
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Qy 7681 ATCTCCTTGCTCATCTTACACCCTGTGTCGATGACGCCCACCATTCATTTATCAGAGC 7740

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Qy  8641 AGGTCTTAACGTTCTCTTTGAAAGAAGAATATTAGGATTCAGAGATATTAAGAGATTCT 8700
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Db  8641 AGGTCTTAACGTTCTCTTTGAAAGAAGAATATTAGGATTCAGAGATATTAAGAGATTCT 8700

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Qy  8821 TAAGTCAGGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAATATTTCAGGCTTTGT 8880
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Qy  8941 GCAAAATAAAATCAACGAATGGCTGTTTTTATGGGATTTTTTTAACTCTTTATTTA 9000
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Qy  9181 ATAAGTGAAATAGTTAAAGTTAGGAACGATCCCAGTTATAAGGAAGCACAAAGAATAATGACC 9240
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Db  9361 AGTATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAA 9420

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Db  9421 TAGGGCCCAGCCTATATTAATTTATCAATAAATGCCAG 9458
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Qy  7681 ATCTCCTGCTCATCTTACACCCTGTGTCAGCAGCCCACCATTCATTTATCAGAGC 7740
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Qy  7741 AAAGGCTCTCCCACTATTCTGGTTCACCCCCTACTTAGCCAGATATACAAGAATATCTG 7800
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Qy  7921 CAAAACACAGTTCTCTTAATTCTCCCAAGAAACCCAGAATGTGACTGCTCACCTCTCTAAG 7980
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Qy  8161 ATTCTAAATTTACTATTCTCAAAGAAATATATTCAGTCAGTAGTGGGGAAAATAGGAT 8220
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APPLICANT: Anne Mette Buhl Hertz
APPLICANT: Jorgen Kjems
TITLE OF INVENTION: Methods and kits for diagnosing and
TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
FILE REFERENCE: P34546US01
CURRENT APPLICATION NUMBER: US/10/535,500A
CURRENT FILING DATE: 2005-05-18
PRIOR APPLICATION NUMBER: DK/PA 200201792
PRIOR FILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 1
LENGTH: 19999
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: gene
LOCATION: 40000-60000
OTHER INFORMATION: Sequence of ac063949.emhum
US-10-535-500A-1

Query Match    100.0%;  Score 9458;  DB 1;  Length 19999;
Best Local Similarity 100.0%;  Pred. No. 1.6e-86;
Matches 9458;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Db 10451 AACCAAAATTGCTTGCTTCGTCATTCTATGGAACCACTGAGAGTTTTACTTGTGCTTA 10510
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Qy 1561 AAATTTTGAATAGTAAACAGAGTGTCAACTTCATGCTGGAATATTTTTGGGCTTTTAGA 1620
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Db 10751 GGAGTAACAAATGATCCACTCTGGGTGTTGAAAACACCAATAAGCCTGCTTCCAGGAAG 10810

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Db 10811 TGCCTAAGACGAGCTGGCTCAGCTTGCTGGGTCACAGCATGTAAGGAAACTGCTGGGCT 10870

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Db 10991 ACTTTGTCAAATTTATTTTCATAAATAACCCAAATATGTATACCACTATTATCCTACC 11050

Qy 2101 TTAAAGAGGAGAAACTGAGCTCTAAAGTTAAATATCTAACCCAAGTTAAGACTGCTAG 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11051 TTAAAGAGGAGAAACTGAGCTCTAAAGTTAAATATCTAACCCAAGTTAAGACTGCTAG 11110

Qy 2161 TCACCCTAGGCTATTAACTCAGGCAGTCTAACTCAGGTATAATAACATTATGCTACTGT 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11111 TCACCCTAGGCTATTAACTCAGGCAGTCTAACTCAGGTATAATAACATTATGCTACTGT 11170

Qy 2221 TGCAGCTTTGACTACTGAATTATAACGTCATGCTATCTAACTAAAAAGCTAAGGGAA 2280
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Db 11171 TGCAGCTTTGACTACTGAATTATAACGTCATGCTATCTAACTAAAAAGCTAAGGGAA 11230

Qy 2281 ATAAAATGAGCCATAGGGCTCAATTTCATAAAAGGAGGAGAAAATACTGGGGAAAAGTGAT 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11231 ATAAAATGAGCCATAGGGCTCAATTTCATAAAAGGAGGAGAAAATACTGGGGAAAAGTGAT 11290

Qy 2341 AATGCAGAGTTTAAAATATTTTGTAAAAGTGCCAGAAGTGAGTATAAACAAGTGTGACC 2400
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Db 11291 AATGCAGAGTTTAAAATATTTTGTAAAAGTGCCAGAAGTGAGTATAAACAAGTGTGACC 11350

Qy 2401 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAGAAGGAGGAGGTAAAAAAAAGAGGAGGTCTGAGAAAT 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11351 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAGAAGGAGGAGGTAAAAAAAAGAGGAGGTCTGAGAAAT 11410

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Qy 2461 AGAAATATCAGAGGAAGGAAGAAATAAAGGAGGGTGAGAGTAAATTCTCTTTTAGCATTCAGA 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11411 AGAAATATCAGAGGAAGGAAGAAATAAAGGAGGGTGAGAGTAAATTCTCTTTTAGCATTCAGA 11470

Qy 2521 TTCCACAGATTCCACAAATCACATTCTTTTTACCAACTAGGAAAAATAACACTTGA 2580
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Db 11471 TTCCACAGATTCCACAAATCACATTCTTTTTACCAACTAGGAAAAATAACACTTGA 11530

Qy 2581 CCTAACATTCATTGCAGTTAGCTAAGGATGCTAGAAAAACTATGTTGCAGTGGTTTGC 2640
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Db 11531 CCTAACATTCATTGCAGTTAGCTAAGGATGCTAGAAAAACTATGTTGCAGTGGTTTGC 11590

Qy 2641 TCTAATTTCTTCAGGAATAGAGAAAAGATCAGAAAAGATCAGAAGGAAGAGAAAGGAAA 2700
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Db 11591 TCTAATTTCTTCAGGAATAGAGAAAAGATCAGAAAAGATCAGAAGGAAGAGAAAGGAAA 11650

Qy 2701 CTATCAGAAAAATACAGAATTGGAGTAGGATAATAACATATTTGGGTGAAGGTAAAATTT 2760
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Db 11651 CTATCAGAAAAATACAGAATTGGAGTAGGATAATAACATATTTGGGTGAAGGTAAAATTT 11710

Qy 2761 TATATTGTAATCTAAGTATCTTGCTACTTCAGTTTGGTCCCTGGAACAGCAGCATCAGA 2820
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Db 11711 TATATTGTAATCTAAGTATCTTGCTACTTCAGTTTGGTCCCTGGAACAGCAGCATCAGA 11770

Qy 2821 ATCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGTCCCATCCCAGACTCACTGAATC 2880
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Qy 2881 AGAATATAAATACTGACAAGATGCCCCGGGATTCATATGCACAGTAGAGCTGGCGAAGTT 2940
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Qy 2941 CCATTGTAGCCTGTGATTGTTTCTGCAACTTAGTATTTCGAGTTTCCCAAGGAAGAA 3000
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Db 11891 CCATTGTAGCCTGTGATTGTTTCTGCAACTTAGTATTTCGAGTTTCCCAAGGAAGAA 11950

Qy 3001 AACCCAGGCCTTAGCTTCTGGCCAGACTTGTGTTCTTCCTTACTTACTAGCTGCATGACT 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11951 AACCCAGGCCTTAGCTTCTGGCCAGACTTGTGTTCTTCCTTACTTACTAGCTGCATGACT 12010

Qy 3061 CATGAGCAAGGAAATCAAACTTATGTGCCTGAGTTTCCTCATCTATAAAAATGGAGACTA 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 12011 CATGAGCAAGGAAATCAAACTTATGTGCCTGAGTTTCCTCATCTATAAAAATGGAGACTA 12070

Qy 3121 TAATAATCATCTCCTAGGCTTGTTTGAGGATGTCAACAAATGCTCCTTTCATTCCTCT 3180
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Db 12071 TAATAATCATCTCCTAGGCTTGTTTGAGGATGTCAACAAATGCTCCTTTCATTCCTCT 12130

Qy 3181 ATTTACAGACCTGCCGCAGCAATTCTGCTAGCAGCCTTTGTGCTATATCTGTTTCTA 3240
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Db 12131 ATTTACAGACCTGCCGCAGCAATTCTGCTAGCAGCCTTTGTGCTATATCTGTTTCTA 12190

Qy 3241 AACTTAGTAATTGAGTGTGATCTGGAGACTAACTCTGAAATAAATAAGCTGATTATTAT 3300
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Db 12191 AACTTAGTAATTGAGTGTGATCTGGAGACTAACTCTGAAATAAATAAGCTGATTATTAT 12250

Qy 3301 TTATTTTCTCAAAACAACAACAGAATACGATTTAGCAAATTACTTCTTAAGTATATTATTAC 3360
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Db 12251 TTATTTTCTCAAAACAACAACAGAATACGATTTAGCAAATTACTTCTTAAGTATATTATTAC 12310

Qy 3361 ATTTCTATATTCTCCTACCCTGAGTTGATGTGTGAGCAATATGTCACTTTCATAAAGCCA 3420
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Db 12311 ATTTCTATATTCTCCTACCCTGAGTTGATGTGTGAGCAATATGTCACTTTCATAAAGCCA 12370

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Db  13271  TCATGAATGGCTGTCAAAATGATTAGTTTAAAAACCTTTCTTGCAGATACGTATGGCA   13330
Qy   4381  CCCTAAAACTGTATTAGAAAAAAGTAAGTACTCGTGTAGTGTGAAAAATTCTTAAAGGAC   4440
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Db  13331  CCCTAAAACTGTATTAGAAAAAAAGTAAGTACTCGTGTAGTGTGAAAAATTCTTAAAGGAC  13390
Qy   4441  ACCCTCTTTACAAACTCACAAAAACAGCCTTTGGAATACCCACATGAAGTAGCTGTTGT    4500
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Db  13391  ACCCTCTTTACAAACTCACAAAAACAGCCTTTGGAATACCCACATGAAGTAGCTGTTGT   13450
Qy   4501  TATTGCTTCTATATACCTACATCTTGTCTATTATAAAAAGACTGGTTTTGGCAGGTGT    4560
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Db  13451  TATTGCTTCTATATACCTACATCTTGTCTATTATAAAAAGACTGGTTTTGGCAGGTGT   13510
Qy   4561  GGTGGCTCACACCTGTAATTCCAGCACTTTGGGAGGCCAAGGCGGGCGGATCACCTGAGA   4620
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Db  13511  GGTGGCTCACACCTGTAATTCCAGCACTTTGGGAGGCCAAGGCGGGCGGATCACCTGAGA  13570
Qy   4621  TCAGGAGTTCAGGACCAGCCTGATCAATATGTGAAACCCAGTCTTACTGAAAATACAA    4680
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Db  13571  TCAGGAGTTCAGGACCAGCCTGATCAATATGTGAAACCCAGTCTTACTGAAAATACAA   13630
Qy   4681  AAATCACCCGGGTGGTGACGGCGCCTGAGTCCCAGCTACTCGGGTAGCTGAGGCAG     4740
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Db  13631  AAATCACCCGGGTGGTGACGGCGCCTGAGTCCCAGCTACTCGGGTAGCTGAGGCAG    13690
Qy   4741  GAGAATCACTTGAACTCAGGAGGTCAGAGGTTGCAGTGAGCTGAGATCATGCCACTGCACT  4800
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Db  13691  GAGAATCACTTGAACTCAGGAGGTCAGAGGTTGCAGTGAGCTGAGATCATGCCACTGCACT 13750
Qy   4801  CCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAAAAAAACTGTTTT   4860
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Db  13751  CCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAAAAAAACTGTTTT  13810
Qy   4861  TCAACAGCTATTCCCACCCCTCTGCATGGAAAATATTCACCCAGTCAATTGTTTCCTAGT   4920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  13811  TCAACAGCTATTCCCACCCCTCTGCATGGAAAATATTCACCCAGTCAATTGTTTCCTAGT  13870
Qy   4921  TTGGGTAATGGCCCCTCTGGGCAGGACTGGAGTGGGGCACACAGGAGAGCTGCAAACTAT   4980
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Db  13871  TTGGGTAATGGCCCCTCTGGGCAGGACTGGAGTGGGGCACACAGGAGAGCTGCAAACTAT  13930
Qy   4981  GTTTAGAAGCATGTCTGGGAAATGTCATGCAAGAAAAGACATATTTAAAGGTAGGCTTTG   5040
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Db  13931  GTTTAGAAGCATGTCTGGGAAATGTCATGCAAGAAAAGACATATTTAAAGGTAGGCTTTG  13990
Qy   5041  CATGAATGGAAAAGGAGGAGTAATTCTATGTAGAGCCAGAGCCTCTTACTTGCAGTGCAGAGA  5100
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Db  13991  CATGAATGGAAAAGGAGGAGTAATTCTATGTAGAGCCAGAGCCTCTTACTTGCAGTGCAGAGA 14050
Qy   5101  AGCAAAGTTGGGGAGGCAAGCAAGGAATTATGCTTTTCATCAGGCAAATTTGCAGGTAGGAG  5160
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Db  14051  AGCAAAGTGGGGGAGGCAAGCAAGGAATTATGCTTTTCATCAGGCAAATTTGCAGGTAGGAG 14110
Qy   5161  GATTGGCTCAGTCATCTTGGCTGAGGCTCATGAAACCAGGTGTAAAGAAAGTGGACTAGA   5220
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Db  14111  GATTGGCTCAGTCATCTTGGCTGAGGCTCATGAAACCAGGTGTAAAGAAAGTGGACTAGA  14170
Qy   5221  TTAATTTCATCCATTACAGGAAGAGGAGCCGTGAAAGATAATCCAGAAATCATTGGGATT   5280
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Db  14171  TTAATTTCATCCATTACAGGAAGAGGAGCCGTGAAAGATAATCCAGAAATCATTGGGATT  14230
Qy   5281  TGATGGTAGAAGGTATTTTGGGACTATTCCATTGAAATGAGGAAGGTACCTGACATTCTT   5340
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Qy   3421  GGTATACATTATGGACAGGTAAGTAAAAAACATATTATTTATTCTACGTTTTTGTCCAAA   3480
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Db  12371  GGTATACATTATGGACAGGTAAGTAAAAAACATATTATTTATTCTACGTTTTTGTCCAAA  12430
Qy   3481  AATTTTAAATTTCAACTGTTGGGCGTGTGTGTAATGTAAAACAAACTCAGTACAGTAG    3540
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db  12431  AATTTTAAATTTCAACTGTTGCGCGTGTGTGTAATGTAAAACAAACTCAGTACAGTAG   12490
Qy   3541  TATTCAGTACAGTATTTAAGCCCCTGTACTTAAACATATTCCTCGTACCCAATGAAGTTAC   3600
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Db  12491  TATTCAGTACAGTATTTAAGCCCCTGTACTTAAACATATTCCTCGTACCCAATGAAGTTAC  12550
Qy   3601  ATGAAAAGGCAAATTTGTGTGAGATATCGTAGATGGAAGTAAATTAGTTCTTTATGTTCCCC  3660
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Db  12551  ATGAAAAGGCAAATTTGTGTGAGATATCGTAGATGGAAGTAAATTAGTTCTTTATGTTCCCC 12610
Qy   3661  ACAAATTGAAATGCATTCAAAAACTCGTGTGTGTATGTGTGTGTGACAGAGTGTGT     3720
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Db  12611  ACAAATTGAAATGCATTCAAAAACTCTGTGTGTATGTGTGTGTGTGACAGAGTGTGT    12670
Qy   3721  GTGAGAGGAGACAGAGAGATACGCTTTGGTTGCCTCCATAAGCTGGCTGCCTCTATGATTAA  3780
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Db  12671  GTGAGAGAGAGACAGAGAGATACGCTTTGGTTGCCTCCATAAGCTGGCTGCTATGATTAA   12730
Qy   3781  TAAGACCAAGTTTCTAAGAAAATGAGATCATAACAAAAGCCCTCTTTATGACTATCTT    3840
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Db  12731  TAAGACCAAGTTTCTAAGAAAATGAGATCATAACAAAAGCCCTCTTTATGACTATCTT   12790
Qy   3841  TTATCAGGGGCAAAAAGGAAAGAGACAAAACAGCATGAAATGATGAGACCAAGTGATGAA   3900
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Db  12791  TTATCAGGGGCAAAAAGGAAAGAGACAAAACAGCATGAAATGATGAGACCAAGTGATGAA  12850
Qy   3901  AATTCATTCACAATGATTGCTTCAAGAGTAATTTCTCTGGGTAATTCAGCAGCCTGT    3960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  12851  AATTCATTCACAATGATTGCTTCAAGAGTAATTTCTCTGGGTAATTCAGCAGCCTGTT  12910
Qy   3961  ACTATGGCTCTCTGGAGTGATAGCTAATG     AAGTGAAGCCTCTAAAGTGGATTATCCTG   4020
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Db  12911  ACTATGGCTCTCTGGAGTGATAGCTAATGTAAATGAAGCCTCTAAAGTGGATTATCCTG  12970
Qy   4021  ACAAGAATATACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCAATTCGGGGAAAAT   4080
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Qy   4081  CAAAAGAATAAAATATTCTTTTTTTTTTTAAAGTTAATGACCTACGATCCATTTCTTCC   4140
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Db  13031  CAAAAGAATAAAATATTCTTTTTTTTTTTAAAGTTAATGACCTACGATCCATTTCTTCC  13090
Qy   4141  CTGACTAACAAGCAGCAAGCACTTAAAAAATATCCAGCCAGGATGAAATAGAAACCCACCT   4200
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Db  13091  CTGACTAACAAGCAGCAAGCACTTAAAAAATATCCAGCCAGGATGAAATAGAAACCCACCT  13150
Qy   4201  GACTTGTTAATATTTTGTTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTTGAAT    4260
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Db  13151  GACTTGTTAATATTTTGTTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTTGAAT   13210
Qy   4261  GATCTTGGCAAATGTCTCGAATTATTTTGCCAACTTTCTTTATCTTGGAAAAAAAGTT    4320
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Db  13211  GATCTTGGCAAATGTCTCGAATTATTTTGCCAACTTTCTTTATCTTGGAAAAAAAGT    13270
Qy   4321  TCATGAATGGGTGTCAAAATTGATTAGTTTAAAAACCTTTCTTGCAGATACGTATGGCA   4380
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Db 14231 TGATGGTAGAAGGTATTTGGGACTATTCCATTTGAAATGAGAAGGTACCTGACATTCTT 14290

Qy  5341 TGAATTCCTTCAAGCAAAGGATTAAATTTACCCATGAGTTGACTCAGAAAAAACATAAA 5400
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Db 14291 TGAATTCCTTCAAGCAAAGGATTAAATTTACCCATGAGTTGACTCAGAAAAAACATAAA 14350

Qy  5401 AAGTATTGTTGCTCTGCTCAGAGTTTATCTAACTCATTCTCTACTTCTTATTCCATGATG 5460
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Qy  5581 CCATGGAAGGCAGTCATTAAGATGTCCCATGCGAGTGAACTTTCCAGGGTTCCCAGCTT 5640
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Db 14531 CCATGGAAGGCAGTCATTAAGATGTCCCATGCGAGTGAACTTTCCAGGGTTCCCAGCTT 14590

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Db 14591 CTGCATCCTCCCTGTCCCTCAATTCCATTGGTGATGACAATGTCTCTCCCATCAGC 14650

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Qy  5761 CCAGTAATGCCTGATTGGCCCCTTATCCTAAAGGCTTAAACTGGAGGAAGGAAGCTAAAC 5820
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Db 14831 GACTAGTATGTGGCAGGCAGTGCCCTTTATTTAGGCAGGGAGAGTTGATGGGGGGGGCG 14890

Qy  5941 GGGTTCACACATCTTAAAGAGGTGCTATCTCCTCCTATATAAATCATGTAAGTCAAGAGA 6000
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Db 14891 GGGTTCACACATCTTAAAGAGGTGCTATCTCCTCCTATATAAATCATGTAAGTCAAGAGA 14950

Qy  6001 GTAAGGAATTGTCTTGTTGGTTATATTCAGGGGATTAGAGTATACAGTATAGAAGATCCC 6060
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Db 14951 GTAAGGAATTGTCTTGTTGGTTATATTCAGGGGATTAGAGTATACAGTATAGAAGATCCC 15010

Qy  6061 AAGAAACCTTGGGATCATATTTAGACTAAGAAGTGCCAATACCGCCGGGCGGTGGCTCA 6120
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Db 15011 AAGAAACCTTGGGATCATATTTAGACTAAGAAGTGCCAATACCGCCGGGCGGTGGCTCA 15070

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Db 15071 CGCCTGTAATCCCAGCACTTTGAGAGGCCGAGGTGGGCGGATCACAAGGTCAGGAGATTG 15130

Qy  6181 AGACCGTCCTGGCTAACGTGGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTAGCCG 6240
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Db 15131 AGACCGTCCTGGCTAACGTGGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTAGCCG 15190
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Qy  6241 GGCGTGGTGGGCGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGTG 6300
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Db 15191 GGCGTGGTGGGCGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGTG 15250

Qy  6301 TGAACTCAGGAGGCGGAGCTTGCAGTCAGCCGAGATTGCCCCAATGCACTCCAGCCTGGG 6360
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Db 15371 AGAGCCAAATCATGAACATAAGCTAAACAAATGTTGGCAGTGTAGCCTAGTGGTTAAGAG 15430

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Db 15431 AGCAGACTCTTAACTAGACACACTGACTCCATGTCCTCACTGAGACCCTCACTGTGTGGGG 15490

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Db 15491 TTCTAATTAACCCCTGTTACTTACCAGTGGCAGTCTTAAGGCATTCCTTAAGTTCGTTGT 15550

Qy  6601 GCCCCAATTTGTTCATCTGTAGAAGGGGTAGGATGACAGTAGTGTTTACTTTATAGGCTT 6660
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Db 15551 GCCCCAATTTGTTCATCTGTAGAAGGGGTAGGATGACAGTAGTGTTTACTTTATAGGCTT 15610

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Qy  6721 AGAGTTGTTAAACACTTAAGAACTGATTACTTGGATCGATCAAACTGACAGCTCTCAATAA 6780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 15671 AGAGTTGTTAAACACTTAAGAACTGATTACTTGGATCGATCAAACTGACAGCTCTCAATAA 15730

Qy  6781 CTGGAAATGATCAAGGATCAGGCCCTGGAATATAAGGCAGGTCTACATGAAGGCAAAAATGT 6840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 15731 CTGGAAATGATCAAGGATCAGGCCCTGGAATATAAGGCAGGTCTACATGAAGGCAAAAATGT 15790

Qy  6841 TCGTTTCTTTGTTCAGCCCTGTGCCTAGATCAATATCTTAGTGATCATCGTCAGTGATCAAGAAATA 6900
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Db 15791 TCGTTTCTTTGTTCAGCCCTGTGCCTAGATCAATATCTTAGTGATCATCGTCAGTGATCAAGAAATA 15850

Qy  6901 TTGTTGAATGAATCAATGAACATACCGAGTAGTTACATAAAAGAGTTCTGCATGAGTAC 6960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 15851 TTGTTGAATGAATCAATGAACATACCGAGTAGTTACATAAAAGAGTTCTGCATGAGTAC 15910

Qy  6961 AAATCTGGGCAAAGTGACCTCCAAGGAAATTCCACTTTAGATTCGTGATTTCCTTAA 7020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 15911 AAATCTGGGCAAAGTGACCTCCAAGGAAATTCCACTTTAGATTCGTGATTTCCTTAA 15970

Qy  7021 GGAACTGATAAATTGGTGTGATACAATGTAAAAAATGTGCCTATATGATTTGAGAAAAAA 7080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 15971 GGAACTGATAAATTGGTGTGATACAATGTAAAAAATGTGCCTATATGATTTGAGAAAAAA 16030

Qy  7081 CTTATTTTCTCTCCCTCTTTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTCCTTCCTCC 7140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 16031 CTTATTTTCTCTCCCTCTTTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTCCTTCCTCC 16090

Qy  7141 CTCCCTTCCTTCCTTCCTTCCTCCCTTCCTCCTTCTTCTTCTTCTTCTTCTTCTTCTT 7200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 16091 CTCCCTTCCTTCCTTCCTTCCTCCCTTCCTCCTTCTTCTTCTTCTTCTTCTTCTTCTT 16150
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10535500-11_vs_10535500allna.txt

Qy   7201  TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT  7260
           |||||||||||| ||||||| |||||||||||||||||||||||||||||||
Db  16151  TCTTCCTTCTTCTTCTTCTTTCTTCTTCTCTTCTTCTCTTCTTCTTCTTCTTCTTCTT   16210

Qy   7261  CTTCCTTCTTCTTGTGCCTTCTTCTTCTTCTTCTTCTCTGTCCTTCTTCTTCTTCTTCCT  7320
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Db  16211  CTTCCTTCTTGTGCCTTCTTCTTCTTCTCTCTGTCCTTCTTCTTCTTCTTCTTCCT    16270

Qy   7321  TCTTCTTCTGCCTTCTCTTCTTCTGTTTCTTCTTCTTTCTTTCCTTCTTTCCTTCTTAA  7380
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  16271  TCTTCCTCTGCCTTCTCTTCTTCTGTTTCTTCTTCCTTTCCTTTCCTTTCCTTAA     16330

Qy   7381  GCAGACCATGTCTGTTAGATGAATGCCTTTTCTAGTTAAAAGGTAAACAGGAAAGTGA    7440
           |||||||||||||||||||||||||||||| |||||||||||||||||||
Db  16331  GCAGACCATGTCTGTTAGATGAATGCCTTTTCTAGTTAAAAGGTAAACAGGAAAGTGA   16390

Qy   7441  AGACAAATTATCAAGGGTCTCCAGTCATCTCCACATGTTCTTAATCATTTATCTTCTTTA  7500
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16391  AGACAAATTATCAAGGGTCTCCAGTCATCTCCACATGTTCTTAATCATTTATCTTCTTTA 16450

Qy   7501  CAGTTCATATCTCCAGGCCTTCATTGGGTCAGGTGGCATTTGCTGCCCTTATGTG      7560
           ||||||||||||||||||||||||||||||||||||||||||||||
Db  16451  CAGTTCATATCTCCAGGCCTTCATTGGGTCAGGTGGCATTTGCTGCCCTTATGTG     16510

Qy   7561  TGTGACAAGTGAAAATAAGGAAGAAAAAAACTCAAGTGAAGAAATCAGAAATCTGCGCA   7620
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16511  TGTGACAAGTGAAAATAAGGAAGAAAAAAACTCAAGTGAAGAAATCAGAAATCTGCGCA  16570

Qy   7621  GCAGTTCCTGGGCGTTCAGCTGCTTCCCACATCACCTGCCTCATCCAAGCCCAGCATCC  7680
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  16571  GCAGTTCCTGGGCGTTCAGCTGCTTCCCACATCACCTGCCTCATCCAAGCCCAGCATCC 16630

Qy   7681  ATCTCCTTGCTCATCTCACACCCTGTGTGCATGGAGGCCCACCATTCATTTATCAGAGC  7740
           |||||||||||||||||||||||||||||||||||||||||||||||
Db  16631  ATCTCCTTGCTCATCTCACACCCTGTGTGCATGGAGGCCCACCATTCATTTATCAGAGC 16690

Qy   7741  AAAGGCTCTCCCACATATTCTGGTTCACCCCCTACTAGCCAGATATACAAGAAAATCTG  7800
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  16691  AAAGGCTCTCCCACATATTCTGGTTCACCCCCTACTAGCCAGATATACAAGAAAATCTG 16750

Qy   7801  CACGGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTATCGCACC  7860
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16751  CACGGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTATCGGACC 16810

Qy   7861  AAGGACAGACGATCTCCCAGCAAGAATGACAGAAAGACTAACTGCGCCCCAAATCTCCCTC 7920
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16811  AAGGACAGACGATCTCCCAGCAAGAATGACAGAAAGACTAACTGCGCCCCAAATCTCCCTC 16870

Qy   7921  CAAAACACAGTTCTCTAATTCTCCCAAGAAAACCAGAATGTGACTGCTCACCTCTCTAAG  7980
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db  16871  CAAAACACAGTTCTCTAATTCTCCCAAGAAAACCAGAATGTGACTGCTCACCTCTCTAAG 16930

Qy   7981  GACCTGAAAACAACTGGCCATTTCAGCTATTTAAATCAACTTAAAAAATCCAACCGCCA   8040
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  16931  GACCTGAAAACAACTGGCCATTTCAGCTATTTAAATCAACTTAAAAAATCCAACCGCCA  16990

Qy   8041  AAATATTAAACCATTTTGGTTGGAATGATAACATAACCTGCTGACAGTTGCTTCTG     8100
           ||||||||||||||||||||||||||||||||||||||||||||||
Db  16991  AAATATTAAACCATTTTGGTTGGAATGATAACATAACCTGCTGACAGTTGCTTCTG    17050

Qy   8101  CTAGGTGCAAAAATGGAAAAAAAAATACTTCTAATCAGGTCAAATCACTCACCTTTGGG  8160
           |||||||||||||||||||||||||||||||||||||||||||||||
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10535500-11_vs_10535500allna.txt

Db  17051  CTAGGTGCAAAAATGGAAAAAAAAATACTTCTAATCAGGTCAAATCACTCACCTTTGGG  17110

Qy   8161  ATTCTAAATTTACTCATATTCTCAAAGAAATATATTCAGTCATAGTGGGGAAAATAGGAT  8220
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17111  ATTCTAAATTTACTCATATTCTCAAAGAAATATATTCAGTCATAGTGGGGAAAATAGGAT 17170

Qy   8221  TATTCCTTTAGCTCGATAAGGCAACCAGCAAGTTCTTCCTTCAAATCTTGACATTTAATCAA 8280
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17171  TATTCCTTTAGCTCGATAAGGCAACCAGCAAGTTCTTCCTTCAAATCTTGACATTTAATCAA 17230

Qy   8281  TCAGAAATTGATTTTTGGAAAACTGTTCCTATGAAGCTATCTCTGCCTGAAGGATTTT   8340
           |||||||||||||||||||||||||||||||||||||||||||||||
Db  17231  TCAGAAATTGATTTTTGGAAAACTGTTCCTATGAAGCTATCTCTGCCTGAAGGATTTT  17290

Qy   8341  CTTTTACAATCCAGACTATAGAAGGAAATTCACAACCTGGACTTCACCTCCATTGGTCA  8400
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  17291  CTTTTACAATCCAGACTATAGAAGGAAATTCACAACCTGGACTTCACCTCCATTGGTCA 17350

Qy   8401  GAGTTTACTGACCAATTCCCACCTCTGCCTACACCTAACGGAAGTTATGCCTGTTT    8460
           |||||||||||||||||||||||||||||||||||||||||||||
Db  17351  GAGTTTACTGACCAATTCCCACCTCTGCCTACACCTAACGGAAGTTATGCCTGTTT   17410

Qy   8461  CTCTTCACATACCCCAACAGTTACAAATGGTTGTATATTAAGCATCTTTATTTGTG    8520
           |||||||||||||||||||||||||||||||||||||||||||||
Db  17411  CTCTTCACATACCCCAACAGTTACAAATGGTTGTATATTAAGCATCTTTATTTGTG   17470

Qy   8521  GCCTCTGATTACATGGTCCCCTAAATTTGACCTAATCACAAAAGAATGGTAAAATTTCT   8580
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  17471  GCCTCTGATTACATGGTCCCCTAAATTTGACCTAATCACAAAAGAATGGTAAAATTTCT  17530

Qy   8581  TAACATATTAATAATATTTGTTTATGTGTCAATATCTTAGCATGTATCAATTCAAGACAG  8640
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  17531  TAACATATTAATAATATTTGTTTATGTGTCAATATCTTAGCATGTATCAATTCAAGACAG 17590

Qy   8641  AGGTCTTAACGTTCTCTTTTGAAAGAGAATATTAGGATTCAGAGATATTAAGAGATTCT   8700
           |||||||||||||||||||||||||||||||||||||||||||||||
Db  17591  AGGTCTTAACGTTCTCTTTTGAAAGAGAATATTAGGATTCAGAGATATTAAGAGATTCT  17650

Qy   8701  CCCAGGATCACAGTTAGGTAACAGAGCTGGATTTTAGTCCAGGTCTGTCACAGCTCTAA  8760
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Db  17651  CCCAGGATCACAGTTAGGTAACAGAGCTGGATTTTAGTCCAGGTCTGTCACAGCTCTAA 17710

Qy   8761  CGTATATACACCCTTGTATAAACATGTCACGAATCAGCATAAAGGGATCTTCAGTGATC  8820
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  17711  CGTATATACACCCTTGTATAAACATGTCACGAATCAGCATAAAGGGATCTTCAGTGATC 17770

Qy   8821  TAAGTCAGGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAATATTTCAGGCTTTGT  8880
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Db  17771  TAAGTCAGGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAATATTTCAGGCTTTGT 17830

Qy   8881  GGACCCTATGGTCTCTATCATAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAA  8940
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db  17831  GGACCCTATGGTCTCTATCATAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAA 17890

Qy   8941  GCAAAATATAAACTAACGAATGTGTCGTTTTATGGATTTTTTAACTCTTTATTTA    9000
           ||||||||||||||||||||||||||||||||||||||||||||
Db  17891  GCAAAATATAAACTAACGAATGTGTCGTTTTATGGGATTTTTTAACTCTTTATTTA   17950

Qy   9001  CAAAGCAGGTGGCAGATCAGAACTCACTTATGGCCATAGTTCTCTGACCCCTGACCTG    9060
           |||||||||||||||||||||||||||||||||||||||||||||||
Db  17951  CAAAGCAGGTGGCAGATCAGAACTCACTTATGGCCATAGTTCTCTGACCCCTGACCTG   18010

Qy   9061  AGAAAATCTTATATTTATGGACAACATTTAGACTGTGACTTGCCAAGTAAGAACAAGAAG  9120
           |||||||||||||||||||||||||||||||||||||||||||||||||
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                10535500-11_vs_10535500a11na.txt
Db 18011 AGAAAATCTTATATTTATGGACAACATTTAGACTGTGACTTGCCAAGTAAGAACAAGAAG 18070
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy  9121 CTCTGTCAACTGAAGGTCAAGGCTGGAGTTCGAAAGCAAAGAGCTGTCTGGTGTTAATG 9180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18071 CTCTGTCAACTGAAGGTCAAGGCTGGAGTTCGAAAGCAAAGAGCTGTCTGGTGTTAATG 18130

Qy  9181 ATAAGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAGAATAATGACC 9240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18131 ATAAGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAGAATAATGACC 18190

Qy  9241 ATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGGCACTTCTTGTGTTGGTCCA 9300
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Db 18191 ATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGGCACTTCTTGTGTTGGTCCA 18250

Qy  9301 GGGCCAAGTTACCTAATCTCTCCAGGCCCTCCATTTCTTATCATTAAATGAAGATAATAAA 9360
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Db 18251 GGCCAAGTTACCTAATCTCTCCAGGCCTCCATTTCTTATCATTAAATGAAGATAATAAA 18310

Qy  9361 AGTATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAAGCCATGTCAAGCACATAGAA 9420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18311 AGTATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAAGCCATGTCAAGCACATAGAA 18370

Qy  9421 TAGGGCCCAGCCTATATTAATTTATCAATAAATGCCAG 9458
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Db 18371 TAGGGCCCAGCCTATATTAATTTATCAATAAATGCCAG 18408
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RESULT 3
US-10-535-500A-5
; Sequence 5, Application US/10535500A
; GENERAL INFORMATION:
; APPLICANT: Rigshospitalet
; APPLICANT: Henrik Leffers
; APPLICANT: Anne Mette Buhl Hertz
; APPLICANT: Jorgen Kjems
; TITLE OF INVENTION: Methods and kits for diagnosing and
; TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
; FILE REFERENCE: P34546US01
; CURRENT APPLICATION NUMBER: US/10/535,500A
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: DK/PA 200201792
; PRIOR FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 89650
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (0)...(0)
; OTHER INFORMATION: human genome sequence
US-10-535-500A-5

Query Match   100.0%;   Score 9458;   DB 1;   Length 89650;
Best Local Similarity   100.0%;
Matches 9458;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    1 ATTTGAATTGGTGAACTTAGTAAGCAGAGGCTCTCACCAATAAGGCAGGCATCATCC 60
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Db 8951 ATTTGAATTGGTGAACTTAGTAAGCAGAGGCTCTCACCAATAAGGCAGGCATCATCC 9010
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                10535500-11_vs_10535500a11na.txt
Qy   61 AATCTGTCGAAAGCTTGAATAAACATTTGAATAAAACAAAAAGAGGAAGGAAGGAAATTTGCTTCTTTCTTCT 120
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Db 9011 AATCTGTCGAAAGCTTGAATAAACATTTGAATAAAACAAAAAGAGGAAGGAAGGAAATTTGCTTCTTTCTTCT 9070

Qy  121 TGATCTAGTATATCATCTTCCTGCCCTTGGATGTGAGTGGCCTTCAGACTTAAACCA 180
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Db 9071 TGATCTAGTATATCATCTTCCTGCCCTTGGATGTGAGTGGCCTTCAGACTTAAACCA 9130

Qy  181 GGAGTTACACCTTGGCTTCCTGGTTCTCAGTTCTTGGACTTGGACTGAATTACACTG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9131 GGAGTTACACCTTGGCTTCCTGGTTCTCAGTTCTTGGACTTGGACTGAATTACACTG 9190

Qy  241 CCAGGTTTCCTGGTTCTCCAGCTTGCAGATGGCAGATCATGGGACTTCTTGGCCTCCATA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9191 CCAGGTTTCCTGGTTCTCCAGCTTGCAGATGGCAGATCATGGGACTTCTTGGCCTCCATA 9250

Qy  301 ATTGTGTGAGTCAATTTCCATTTATTTATTTACATATCCAGTTATGCATTGCATTGCTTAACAATGGA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9251 ATTGTGTGAGTCAATTTCCATTTATTTATTTACATATCCAGTTATGCATTGCATTGCTTAACAATGGA 9310

Qy  361 GACAGGTTCTGAGAAATGCATTGTTAAGTGATTTCATCATTGTGCAAACATCATAGAGTG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9311 GACAGGTTCTGAGAAATGCATTGTTAAGTGATTTCATCATTGTGCAAACATCATAGAGTG 9370

Qy  421 TAACTACACAAACCTGGACAGCATAGACTACTACACACTCAGCCTACATGGTGTAGCTTG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9371 TAACTACACAAACCTGGACAGCATAGACTACTACACACTCAGCCTACATGGTGTAGCTTG 9430

Qy  481 TAACCTCATGATAAGTATGTATAACATCATGATAAGTATGTATGTATCTACCATATCTAA 540
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Db 9431 TAACCTCATGATAAGTATGTATAACATCATGATAAGTATGTATGTATCTACCATATCTAA 9490

Qy  541 ATGTAGAAAAGTACAGTAAAAATATGGTATAATCTTATGGGATCACCATCATATATGCA 600
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Db 9491 ATGTAGAAAAGTACAGTAAAAATATGGTATAATCTTATGGGATCACCATCATATATGCA 9550

Qy  601 ATCCTTTGTAGACTGAAATGTCATTGTGAGTGACTGTATACGCACACATACACAA 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9551 ATCCTTTGTAGACTGAAATGTCATTGTGAGTGACTGTATACGCACACATACACAA 9610

Qy  661 ACACACAAATATACTATTGGTTCTTTTCTGAAGAGCCCTAATACAATATGTTATA 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9611 ACACACAAATATACTATTGGTTCTTTTCTGAAGAGCCCTAATAOAATATGTTATA 9670

Qy  721 CATTTATATTGACTCTATTTCAAAATTTATGGTTTTGGTGAAACATATGTGGAGATGGGG 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9671 CATTTATATTGACTCTATTTCAAAATTTATGGTTTTGGTGAAACATATGTGGAGATGGGG 9730

Qy  781 CATAGGTGTGTGAACTGGGATAGTGTCCTGCTGATGAATGGGTGGGAGGCATCATTTGGG 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9731 CATAGGTGTGTGAACTGGGATAGTGTCCTGCTGATGAATGGGTGGGAGGCATCATTTGGG 9790

Qy  841 ACAAGCCCAGGGCATCAGCTTATAGATATCAAGAGCTCAACAAGAGCACTTATGGCAAA 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9791 ACAAGCCCAGGGCATCAGCTTATAGATATCAAGAGCTCAACAAGAGCACTTATGGCAAA 9850

Qy  901 ACCTCCCACAAGACCTCTCAGAAGTTGAGAAACTGCTAAAAGTTCTTATGCACAGATGA 960
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Db 9851 ACCTCCCACAAGACCTCTCAGAAGTTGAGAAACTGCTAAAAGTTTCTTATGACAGATGA 9910

Qy  961 CATTTATGGGATAAAATAGGGATTAGCACGGATTCTTAAATACTTTCGAACACTAACCTTC 1020
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10535500-11_vs_10535500allna.txt

Db 10871 ACATGGCCACCATCCTCAGTTGTCCAGATAGATAATCCCATAGCCCCATGGGGAAATAATC 10930

Qy  1981 TTTAATTATGATATAGCTGACACCATTCAAAGCACTAGCTAAGTCCTTTATGTGAATTA   2040
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Db 10931 TTTAATTATGATATAGCTGACACCATTCAAAGCACTAAGTCCTTTATGTGAATTA     10990

Qy  2041 ACTTTTGTCAAATTTATTTTTCATAAATAACCCAAATATGTATACCACTATTATCCTACC  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 10991 ACTTTTGTCAAATTTATTTTTCATAAATAACCCAAATATGTATACCACTATTATCCTACC  11050

Qy  2101 TTAAAGAGGAGAAACTGAGCTCTAAAGTTAAATATCTAACCCAAGTTAAGACTGCTAG   2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11051 TTAAAGAGGAGAAACTGAGCTCTAAAGTTAAATATCTAACCCAAGTTAAGACTGCTAG   11110

Qy  2161 TCACCCTAGGCTATTAACTCAGGCAGTCTAACTCAGGTATAATAACATTATGCTACTGT   2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11111 TCACCCTAGGCTATTAACTCAGGCAGTCTAACTCAGGTATAATAACATTATGCTACTGT   11170

Qy  2221 TGCAGCTTGACTATGCCTGAATTATAACGTCATGCTATCTAACTAAAAAGCTAAGGGAA   2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11171 TGCAGCTTGACTATGCCTGAATTATAACGTCATGCTATCTAACTAAAAAGCTAAGGGAA   11230

Qy  2281 ATAAAATGAGCCATAGGGCTCAATTCATAAAAGGAGAGAAAATACTGGGGAAAAGTGAT   2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11231 ATAAAATGAGCCATAGGGCTCAATTCATAAAAGGAGAGAAAATACTGGGGAAAAGTGAT   11290

Qy  2341 AATGCAGAGTTTAAAATATTTTGTAAAAGTGCCAGAGATTGAGTATAACAAGTGTGACC   2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11291 AATGCAGAGTTTAAAATATTTTGTAAAAGTGCCAGAGATTGAGTATAACAAGTGTGACC   11350

Qy  2401 AAAAAAAAAAAAAAAAAAAAAAAGGAAGAAGGTAAAAAAAGAGGGAGGTCTGAGAAAT   2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11351 AAAAAAAAAAAAAAAAAAAAAAAGGAAGAAGGTAAAAAAAGAGGGAGGTCTGAGAAAT   11410

Qy  2461 AGAAATATCAGAGGAGGAAGAAATAAAGGAGGGTGAGAGTAAATTCTCTTTAGCATTCAGA  2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11411 AGAAATATCAGAGGAGGAAGAAATAAAGGAGGGTGAGAGTAAATTCTCTTTAGCATTCAGA  11470

Qy  2521 TTCCACAGATTCCACAAATCACATTTCTTTTTACCAACTAAGGAAAAATAAACACTTGA   2580
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Db 11471 TTCCACAGATTCCACAAATCACATTTCTTTTTACCAACTAAGGAAAAATAAACACTTGA   11530

Qy  2581 CCTAACATTCATTGCAGTTAGCTAAAGGATGCTAGAAAAAACTATGTTGCAGTGGTTGC   2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11531 CCTAACATTCATTGCAGTTAGCTAAAGGATGCTAGAAAAAACTATGTTGCAGTGGTTGC   11590

Qy  2641 TCTAATTTCTTCAGGAATAGAGAAAAGTGACAAAAAAGATCAGAGAAGGAGAAGGGAAA   2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11591 TCTAATTTCTTCAGGAATAGAGAAAAGTGACAAAAAAGATCAGAGAAGAGAAAGGGAAA   11650

Qy  2701 CTATCAGAAAAATACAGAATTGGAGTAGGATAAAACATATTTGGGTTGAAGGTAAAATT   2760
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Db 11651 CTATCAGAAAAATACAGAATTGGAGTAGGATAAAACATATTTGGGTTGAAGGTAAAATT   11710

Qy  2761 TATATTGTAATCTTAAGTATCTTGCTACTTCAGTTTGGTCCCTGGAACAGCAGCATCAGA  2820
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Db 11711 TATATTGTAATCTTAAGTATCTTGCTACTTCAGTTTGGTCCCTGGAACAGCAGCATCAGA  11770

Qy  2821 ATCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGGTCCCATCCCAGACTCACTGAATC  2880
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Db 11771 ATCTGCCGAGGGCTTGTTAAAAAGGCAGAATCTCAGGTCCCATCCCAGACTCACTGAATC  11830

Qy  2881 AGAATATAAATACTGACAAGATGCCCCGGGATTCCATATGCACAGTAGAGCTGGCGAAGTT  2940
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Qy  1021 ATTTCTACCAGGCAGTGGGGCCCAAGTGCAGGGCCATAGGAAGTACAAGTCTGGGAGAT   1080
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Db  9971 ATTTCTACCAGGCAGTGGGGCCCAAGTGCAGGGCCATAGGAAGTACAAGTCTGGGAGAT   10030

Qy  1081 ACTAGGCTGCACTGTCTGTAGAGAATCTGAAAAAATAATAGAGTCACTGAAATGCAGTTT  1140
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Db 10031 ACTAGGCTGCACTGTCTGTAGAGAATCTGAAAAAATAATAGAGTCACTGAAATGCAGTTT  10090

Qy  1141 GGTATAATTATTGCCATGCATCATAATTCTAAATCATACTAGTGGTCAAATACTCTTCCC  1200
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Db 10091 GGTATAATTATTGCCATGCATCATAATTCTAAATCATACTAGTGGTCAAATACTCTTCCC  10150

Qy  1201 TGAAAAAACATTTTCTTGGTTGAATTCTAAATAATTGTTGTGGTCACCACTGAGCTTTT   1260
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Db 10151 TGAAAAAACATTTTCTTGGTTGAATTCTAAATAATTGTTGTGGTCACCACTGAGCTTTT   10210

Qy  1261 AAATATATAAATACTTCAAGTTGCATATTTTATTACCTGTTCCTTAACAAACATTGA    1320
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Db 10211 AAATATATAAATACTTCAAGTTGCATATTTTATTACCTGTTCCTTAACAAACATTGA    10270

Qy  1321 ATTCAACATGAAAATGATTATGGGCAAACATTCGGGTATACAGTCCCTGACTCTTAAGGAC  1380
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Db 10271 ATTCAACATGAAAATGATTATGGGCAAACATTCGGGTATACAGTCCCTGACTCTTAAGGAC  10330

Qy  1381 TCAGGTAAATACTTAGGGTATTCATGGCCCTAGTCTTTGGGGTACCACATGTTTCTTCT   1440
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Db 10331 TCAGGTAAATACTTAGGGTATTCATGGCCCTAGTCTTTGGGGTACCACATGTTTCTTCT   10390

Qy  1441 TCAAATCACAGATTCAAAATCAAGAATGATAACACAGTGATTGTGTAGACAAAATAAGTG  1500
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Db 10391 TCAAATCACAGATTCAAAATCAAGAATGATAACACAGTGATTGTGTAGACAAAATAAGTG  10450

Qy  1501 AACCAAAATTGCTTGCTTCTGTCATTCATGGAACCACTGAGAGTTTTACTTGTGCTTA   1560
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Db 10451 AACCAAAATTGCTTGCTTCTGTCATTCATGGAACCACTGAGAGTTTTACTTGTGCTTA   10510

Qy  1561 AAATTTGAATAGTAAAACAGAGTGTCAACTTCATGCTGGAATATTTTGGCTTTTAGA    1620
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Db 10511 AAATTTGAATAGTAAAACAGAGTGTCAACTTCATGCTGGAATATTTTGGCTTTTAGA    10570

Qy  1621 CACAATTTAAGTACAGTGAAGTATATTTTACAAGACTAAGTAACATCACTGAAATTACAGC  1680
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Db 10571 CACAATTTAAGTACAGTGAAGTATATTTTACAAGACTAAGTAACATCACTGAAATTACAGC  10630

Qy  1681 TTCTCTTAAAACTGGTATTTGTTATAAAACTAAAGAGCGAATCAAGAAAAAGCATA    1740
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Db 10631 TTCTCTTAAAACTGGTATTTGTTATAAAACTAAAGAGCGAATCAAGAAAAAGCATA    10690

Qy  1741 ATTATTACTGATTATTACAGGATTATTACTGAAAAAGAAATGTACGGAATAGAGGAGGAA   1800
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Db 10691 ATTATTACTGATTATTACAGGATTATTACTGAAAAAGAAATGTACGGAATAGAGGAGGAA   10750

Qy  1801 GGAGTTAACAAATGATCCACTCTGGGTGTTGAAAACACCCAATAAGCCTGCTTCCAGGAAG  1860
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Db 10751 GGAGTTAACAAATGATCCACTCTGGGTGTTGAAAACACCCAATAAGCCTGCTTCCAGGAAG  10810

Qy  1861 TGCCTAAGACAGAGCTGGCTCAGCTTGCTGGGTCACAGCATGTGAAGGAAACTGCTGGGCT  1920
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Qy  1921 ACATGCCACCATCCTCAGTTGTCCAGATAGATAATCCCATAGCCCCATGGGGAAATAATC   1980
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Qy   3841 TTATCAGGGGCAAAAGGAAAGACAAAACAGCATGAAATGATGAGACCAAGTGATGAA 3900
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Qy   3901 AATTCATTCACAATGATTGCTTCAAGAGTAATTTCTCTTGGGTAATTCAGCAGCCTGTT 3960
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Db  13091 CTGACTAACAAGCAGCAAGCACTTAAAAATATCCAGCCAGGATGAAATAGAAACCCACCT 13150

Qy   4201 GACTTGTTAATAT...TTGTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTTGAAT 4260
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Qy   4261 GATCTTGGCAAATGTCTCAATTA...TTTGCCAACTTTTCTTATCTTGGAAAAAAAGT 4320
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Qy   4321 TCATGAATGGGTGTCAAAATTGATTAGTTAAAAACCTTTCTGCAGATACGTATGGCA 4380
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Db  13271 TCATGAATGGGTGTCAAAATTGATTAGTTAAAAACCTTTCTGCAGATACGTATGGCA 13330

Qy   4381 CCCTAAAACTGTATTAGAAAAAAAGTAAGTACTCGTAGTGTGAAAAATTCTTAAAGGAC 4440
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Db  13391 ACCCTCTTTACAAACTCACAAAAACAGCCTTTGGAATACCCACATGAAGTAGCTGTTGT 13450

Qy   4501 TATTGCTTTCTATATACCTACATCTTGTCTATTATAAAAAGACTGGTTTTGGCAGGTGT 4560
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Qy   4561 GGTGGCTCACACCTGTAATTCCAGCACTTTGGGAGGCCAAGGCGGGGATCACCTGAGA 4620
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Db  13511 GGTGGCTCACACCTGTAATTCCAGCACTTTGGGAGGCCAAGGCGGGGATCACCTGAGA 13570

Qy   4621 TCAGGAGTTCAGGACCAGCCTGATCAATATGGTGAAACCCCAGTCTTACTGAAAATACAA 4680
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Db  13571 TCAGGAGTTCAGGACCAGCCTGATCAATATGGTGAAACCCCAGTCTTACTGAAAATACAA 13630

Qy   4681 AAATCACCCGGGTGTGGTGGCGGGCGCCTGTAGTCCCAGCTACTCGGGTAGGCTGAGGCAG 4740
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Qy   4741 GAGAATCACTTGAACTTCAGGAGTTGCCACTGCCACTGCACT 4800
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Db  13691 GAGAATCACTTGAACTTCAGGAGTTGCCACTGCCACTGCACT 13750
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Db  11831 AGAATATAAATACTGACAAGATGCCCCGGGATTCATATGCACAGTAGAGCTGGCGAAGTT 11890

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Db  11891 CCATTGTAGCCTGTGATTGTTTCTGCAACTTAGTATTTCTGAGTTTTCCCAAGGAAGAA 11950

Qy   3001 AACCCAGGCCTTAGCTTCTGGCGAGACTTGTGTTTCTCCTTACTTACTAGCTGCATGACT 3060
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Db  11951 AACCCAGGCCTTAGCTTCTGGCGAGACTTGTGTTTCTCCTTACTTACTAGCTGCATGACT 12010

Qy   3061 CATGAGCAAGGAAATCAAACTTATGTGCCTGAGTTCCTCATCTATAAAATGGAGACTA 3120
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Db  12011 CATGAGCAAGGAAATCAAACTTATGTGCCTGAGTTCCTCATCTATAAAATGGAGACTA 12070

Qy   3121 TAATAATCATCTCCTAGGCTTGTTTGAGGATGTTCAACAAATGCTCCTTTCATTCCTCT 3180
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Db  12071 TAATAATCATCTCCTAGGCTTGTTTGAGGATGTTCAACAAATGCTCCTTTCATTCCTCT 12130

Qy   3181 ATTTACAGACCTGCCGCAGACAATTCTGCTAGCAGCCTTGTGCTATTATCTGTTTTCTA 3240
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Db  12131 ATTTACAGACCTGCCGCAGACAATTCTGCTAGCAGCCTTGTGCTATTATCTGTTTTCTA 12190

Qy   3241 AACTTAGTAATTGAGTGTGATCTGGAGACTAACTCTGAAATAAATAAGCTGATTATTTAT 3300
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Db  12191 AACTTAGTAATTGAGTGTGATCTGGAGACTAACTCTGAAATAAATAAGCTGATTATTTAT 12250

Qy   3301 TTATTTTCTCAAAACAACAGAATACGATTTAGCAAATTACTTCTTAAGATATATTTTAC 3360
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Db  12251 TTATTTTCTCAAAACAACAGAATACGATTTAGCAAATTACTTCTTAAGATATATTTTAC 12310

Qy   3361 ATTTCTATATTCTCCTACCCTGAGTTGATGTGGAGCAATATGTCACTTTCATAAAGCCA 3420
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Qy   3421 GGTATACATTATGGACAGGTAAGTAAAAAAACATATATTATTCTACGTTTGTCCAA 3480
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Qy   3481 AATTTAAATTCAACTGTTGCGCGGTGTGTTGGTAATGTAAACAAACTCAGTACAGTAG 3540
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Qy   3541 TATTCAGTACAGTATTTAAGCCCCTGTACTTAAACATATTCCTCCGTACCAATGAAGCTAC 3600
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Qy   3721 GTGAGAGAGACAGAGAGATAGCGCTTTGGTGCCTCCATAAGCTGGCTGCTATGATTAA 3780
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Qy   3781 TAAGACCAAGTTTCTAAAGAAAATGAGATCATAACAAAAGCCCTCTTTATGACTATCTT 3840
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Db  12731 TAAGACCAAGTTTCTAAAGAAAATGAGATCATAACAAAAGCCCTCTTTATGACTATCTT 12790
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Qy   4801 CCAGCCTGGGTGACAGAGACTCCATCTCAAAAAAAAAAAAAAAAAGACTGGTTT 4860
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Qy   4861 TCAACAGCTATTCCCACCCCTCGCATGGAAATATTCACCCAGTCAATTGTTTTCCTAGT 4920
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Qy   5161 GATTGGCTCAGTCATCTTGGCTGAGGCTCATGAAACCAGGTGTAAAGAAAGTGGACTAGA 5220
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Qy   5221 TTAATTCATCCATTACAGGAAGAGGAGGAGCCGTGAAAGATAATCATTCCAGAAATCATTGGAT 5280
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Db   14171 TTAATTCATCCATTACAGGAAGAGGAGGAGCCGTGAAAGATAATCATTCCAGAAATCATTGGAT 14230

Qy   5281 TGATGGTAGAAGGTATTTTGGGACTATTCCATTGAAAATGAGAAGGTACCTGACATTCTT 5340
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Db   14231 TGATGGTAGAAGGTATTTTGGGACTATTCCATTGAAAATGAGAAGGTACCTGACATTCTT 14290

Qy   5341 TGAATTCCTTCAAGCAAAGGATTAAAATTACCCATGAGTTGACTCAGAAAAAACATAAA 5400
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Qy   5401 AAGTATTGTTGCTCTGCTCAGAGTTTATCTAACTCATTCTCACTTCTTATTCCATGATG 5460
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Qy   14651 CTCATGAAGTTCTCTCATTATTAAAATTGCTTCAGGAAAAAATTTTGAAAAATGTGT 14710
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Db   15071 CGCCTGTAATCCCAGCACTTTGAGAGGCCGAGGTGGGCGGATCACAAGGTCAGGAGATTG 15130

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Qy   6241 GGCGTGGTGGCGGGCGCCTGTAGTCCCAGCTACTCGGGAGGCAGGAGAATGGTG 6300
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Qy   6301 TGAACTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCCCCAATGCCAATACCAGCAGAAAT 6360
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Db   15251 TGAACTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCCCCAATGCCAATACCAGCAGAAAT 15310

Qy   6361 CGACAGAACGAGACTCCGTCAGAACAAAACAAAAGGAAATGCCAATACCAGCAGAAAT 6420
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Qy   6421 AGAGCCAAATCATGAACATAAGCTAAACAAATGTTGGCAGTGTAGCCTAGTGGTTAAGAG 6480
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Db   15371 AGAGCCAAATCATGAACATAAGCTAAACAAATGTTGGCAGTGTAGCCTAGTGGTTAAGAG 15430

Qy   6481 AGCAGACTCTAACTAGAACACTGCACTCCTCACTGTGGGGG 6540
            |||||||||||||||||||||||||||||||||||||||||
Db   15431 AGCAGACTCTAACTAGAACACTGCACTCCTCACTGTGGGGG 15490

Qy   6541 TTCTAATTAACCCGTTCATCGTGTAGAAGGGGTAGGATGACAGTAGTGTTTACTTTATAGGCTT 6600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15491 TTCTAATTAACCCGTTCATCGTGTAGAAGGGGTAGGATGACAGTAGTGTTTACTTTATAGGCTT 15550

Qy   6601 GCCCCAAATTTGTTCATCGTGTAGAAGGGGTAGGATGACAGTAGTGTTTACTTTATAGGCTT 6660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15551 GCCCCAAATTTGTTCATCGTGTAGAAGGGGTAGGATGACAGTAGTGTTTACTTTATAGGCTT 15610

Qy   6661 ACTGTGAGCATTAAATGAGTTAAGTACTACTGTATTGTAAAGTGCTTAAAATGCTGCTCCAAA 6720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||

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Qy   7621  GCAGTTCCTGGGCGTTCAGCTGCTTCCCACATCACCTGCCTCATCAAGCCCCAGCATCC   7680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16571  GCAGTTCCTGGGCGTTCAGCTGCTTCCCACATCACCTGCCTCATCAAGCCCCAGCATCC  16630

Qy   7681  ATCTCCTTGCTCATCTTACACCCGTGTGCATGAGAGGCCCACCATTCATTTATCAGAGC   7740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16631  ATCTCCTTGCTCATCTTACACCCGTGTGCATGACAGGCCCACCATTCATTTATCAGAGC  16690

Qy   7741  AAAGGCTCTCCACTATTCTGGTTCACCCCCCTACTTAGCCAGATACAAGAATATCTG     7800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16691  AAAGGCTCTCCACTATTCTGGTTCACCCCCCTACTTAGCCAGATACAAGAATATCTG   16750

Qy   7801  CACGGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTATCGGACC   7860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16751  CACGGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTATCGGACC  16810

Qy   7861  AAGGACAGATCTCCCAGCAAGAATGACACAGAAAAGACTAACTGCCCCAAATCTCCCTTC   7920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16811  AAGGACAGATCTCCCAGCAAGAATGACACAGAAAAGACTAACTGCCCCCAAATCTCCCTTC  16870

Qy   7921  CAAAACACAGTTCTCTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTAAG     7980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16871  CAAAACACAGTTCTCTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTCTAAG   16930

Qy   7981  GACCTGAAAACAACTGGCCATTTCAGCTATTTAAATCAACTTAAAAATCCAACCGCCA    8040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16931  GACCTGAAAACAACTGGCCATTTCAGCTATTTAAATCAACTTAAAATAACCGCCA     16990

Qy   8041  AAATATTTAAACCATTTTGGTTGGAATGATAACATAACCTGCTGACAGCTGCTTCTG     8100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16991  AAATATTTAAACCATTTTGGTTGGAATGATAACATAACCTGCTGACAGCTGCTTCTG   17050

Qy   8101  CTAGGTGCAAAATGGAAAAAAAATACTTCTAATGCGTCAAATCACTCTACCTTTGGG     8160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17051  CTAGGTGCAAAATGGAAAAAAAATACTTCTAATGCGTCAAATCACTCTACCTTTGGG   17110

Qy   8161  ATTCTAAATTACTCATATTCTCAAAGAAATATATTCAGTCATAGTGGGGAAAATAGGAT   8220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17111  ATTCTAAATTACTCATATTCTCAAAGAAATATATTCAGTCATAGTGGGGAAAATAGGAT  17170

Qy   8221  TATTCCTTAGCTCGATAAGCAACCAGAAGTTCTTCCTCAAATCTTGACATTTAATCAA   8280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17171  TATTCCTTAGCTCGATAAGCAACCAGAAGTTCTTCCTCAAATCTTGACATTTAATCAA  17230

Qy   8281  TCAGAAATTGATTTTGGAAAACTGTTTCCTATGAAGCTATCTCGCTGAGGGATTTT    8340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17231  TCAGAAATTGATTTTGGAAAACTGTTTCCTATGAAGCTATCTCGCTGAGGGATTTT   17290

Qy   8341  CTTTACAATCCAGACTATAGAAGGAAATTCACAACCTGGACTTTCACCTCCATTGGTCA   8400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17291  CTTTACAATCCAGACTATAGAAGGAAATTCACAACCTGGACTTTCACCTCCATTGGTCA  17350

Qy   8401  GAGTTTACTGACCAATTCCCACCTCTGCCTTCACACCTAACGGAAGTTATGCCTGTTT   8460
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17351  GAGTTTTACTGACCAATTCCCACCTCTGCCTTCACACCTAACGGAAGTTATGCCTGTTT  17410

Qy   8461  CTCTTCACATACCCCAACAGTACAAATGGTTGTTATTTAAGCATCTTTTATTTTGTG   8520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17411  CTCTTCACATACCCCAACAGTACAAATGGTTGTTATTTAAGCATCTTTTATTTTGTG   17470

Qy   8521  GCCTCTGATTACATGGTCCCCTAAATTTGACCTAATCACAAAGATTGGTAAAATTTCT   8580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17471  GCCTCTGATTACATGGTCCCCTAAATTTGACCTAATCACAAAGATTGGTAAAATTTCT  17530
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Db  15611  ACTGTGAGCATTAAATGAGTTACTACTGTATTGTAAAGTGCTTAAAATGCTGCTCCAAA  15670

Qy   6721  AGAGTTTGTTAAACACTTAAGAACTGATTTACTTGCATCTAAACTGACAGCTCTCAATAA   6780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15671  AGAGTTTGTTAAACACTTAAGAACTGATTTACTTGCATCTAAACTGACAGCTCTCAATAA  15730

Qy   6781  CTGGAAATGATCAAGCATAGGCCTGGAATATAAGCAGGTCACACGTACAGTGAAGGCAAAATGT   6840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15731  CTGGAAATGATCAAGCATAGGCCCTGGAATATAAGCAGGTCACATGAAGGCAAAAATGT  15790

Qy   6841  TCGTTCTTGTTCAGCCCTGCCTAGATCAATATCTAGTGATCATGCTCAAGAAATA      6900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15791  TCGTTCTTGTTCAGCCCTGCCTAGATCAATATCTAGTGATCATGCTCAAGAAATA    15850

Qy   6901  TTGTTGAATGAATCAATGAACCTACCGAGGTAGTTACATAAAAGAGTTCTGCATGAGTAC   6960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15851  TTGTTGAATGAATCAATGAACCTACCGAGGTAGTTACATAAAAGAGTTCTGCATGAGTAC  15910

Qy   6961  AAATCTGGGCAAAGTGACCTCCAGGAAATTCCACTTTAGATTCTGTGATTTCCTTAA     7020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15911  AAATCTGGGCAAAGTGACCTCCAGGAAATTCCACTTTAGATTCTGTGATTTCCTTAA   15970

Qy   7021  GGAACTGATAAATTGGTGTGATACAAATGTAAAAAATGTGCCTATATGATTTGAGAAAA   7080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15971  GGAACTGATAAATTGGTGTGATACAAATGTAAAAAATGTGCCTATATGATTTGAGAAAA  16030

Qy   7081  CTTATTTCTCTCCCTTTCCTTCCTCCTCCTCCTCCTCCTCCTCCTTTCCTTCC      7140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16031  CTTATTTCTCTCCCTTTCCTTCCTCCTCCTCCTCCTCCTCCTTCCTTCCTCC     16090

Qy   7141  CTCCCTTCCTTCCTCCCCCTCCTTCCTTCTTCTTCTTCTTCCTTCT         7200
           ||||||||||||||||||||||||||||||||||||||||||||||
Db  16091  CTCCCTTCCTTCCTCCCCCTCCTTCCTTCTTCTTCTTCTTCTTCTT       16150

Qy   7201  TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTTT          7260
           ||||||||||||||||||||||||||||||||||||||||||||||
Db  16151  TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTTT        16210

Qy   7261  CTTCCTTCTTGTGCCTTCTTCTTCTTCTCTGTCCTTCTTTCTTCTCCT        7320
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  16211  CTTCCTTCTTGTGCCTTCTTCTTCTTCTCTGTCCTTCTTTCTTCTCCT      16270

Qy   7321  TTCTTCTTCTTCTGCCTTCTTCTCTGTTTTCTTCTTTCTTTTCCTTAA        7380
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  16271  TTCTTCTTCTTCTGCCTTCTTCTCTGTTTTCTTCTTTCTTTTCCTTAA      16330

Qy   7381  GCAGACCATGTCTGTTAGATGAATGCCTTCTAGTTAAAAGGTTAAACAGGAAAGTGA      7440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16331  GCAGACCATGTCTGTTAGATGAATGCCTTCTAGTTAAAAGGTTAAACAGGAAAGTGA    16390

Qy   7441  AGCACAATTATCAAGGGTCTCCAGTCATCTCCACATGTCTTAATCATTCATTCTTTTA    7500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16391  AGCACAATTATCAAGGGTCTCCAGTCATCTCCACATGTTCTTAATCATTCATTCTTTTA  16450

Qy   7501  CAGTTTCATATCTCCAGGCCTTCATTGGGTCAGGTCAGGTTCGGCTGCCCTTTATGTG   7560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16451  CAGTTTCATATCTCCAGGCCTTTCATTGGGTCAGGTCAGGTTCGGCTGCCCTTTATGTG  16510

Qy   7561  TGTGACAAGTGAAAATAAGGAAAGAAAAAACTCAAGTGAAGAAAATCAGAATCTGCGCA   7620
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Db  16511  TGTGACAAGTGAAAATAAGGAAAGAAAAAACTCAAGTGAAGAAAATCAGAATCTGCGCA  16570
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US-10-535-500A-4
; Sequence 4, Application US/10535500A
; GENERAL INFORMATION:
;   APPLICANT: Rigshospitalet
;   APPLICANT: Henrik Leffers
;   APPLICANT: Anne Mette Buhl Hertz
;   APPLICANT: Jørgen Kjems
;   TITLE OF INVENTION: Methods and kits for diagnosing and
;   TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
;   FILE REFERENCE: P34546US01
;   CURRENT APPLICATION NUMBER: US/10/535,500A
;   CURRENT FILING DATE: 2005-05-18
;   PRIOR APPLICATION NUMBER: DK/PA 200201792
;   PRIOR FILING DATE: 2002-11-19
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 6209
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-535-500A-4

Query Match   49.2%; Score 4649.5; DB 1; Length 6209;
Best Local Similarity 66.7%; Pred. No. 5.8e-42;
Matches 6209; Conservative 0; Mismatches 0; Indels 3099; Gaps 1;

Qy   151 GGATGTGAGTGGGCCTTCAGACTTAAACCAGGAGTTACACCCTTGGCTTCCCTGGTTCTC 210
         ||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGATGTGAGTGGGCCCTTCAGACTTAAACCAGGAGTTACACCCTTGGCTTCCCTGGTTCTC 60

Qy   211 AGTTCTTGGACTGGACTGAATTACACTGCCAGGTTCCTGGTTCTCCAGCTTGCAGAT 270
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Qy   271 GGCAGATCATGGGACTTCTTGGCCTCCATAATTGTGTGAGTCAATTTCCATTTATTTAC 330
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Db   121 GGCAGATCATGGGACTTCTTGGCCTCCATAATTGTGTGAGTCAATTTCCATTTATTTAC 180

Qy   331 ATATCCAGTTATGCATTGCTTAACAATGGAGACAGGTTCTGAGAAATGCATTGTTAAGTG 390
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATATCCAGTTATGCATTGCTTAACAATGGAGACAGGTTCTGAGAAATGCATTGTTAAGTG 240

Qy   391 ATTTCATCATTGTGCAAACATCATAGAGTGTAACTACACAAACCTGGACAGCAGCATAGACTA 450
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATTTCATCATTGTGCAAACATCATAGAGTGTAACTACACAAACCTGGACAGCAGCATAGACTA 300

Qy   451 CTACACATCTAGGCTACATGGTGTGAGCTTGTAGCCTGTGATAAGTATGTATAACATCAT 510
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTACACATCTAGGCTACATGGTGTGAGCTTGTAGCCTGTGATAAGTATGTATAACATCAT 360

Qy   511 GATAAGTATGTATGTATCTACCATATCTAAATGTAGAAAAGGTACAGTAAAAATATGGTA 570
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GATAAGTATGTATGTATCTACCATATCTAAATGTAGAAAAGGTACAGTAAAAATATGGTA 420

Qy   571 TAATCTTATGGATCACCATCATATATGCAATCCTTTGTGAGACTGAAATGTCATTGTGTA 630
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TAATCTTATGGATCACCATCATATATGCAATCCTTTGTGAGACTGAAATGTCATTGTGTA 480

Qy   631 GTGCATGACTGTATACGCACACATACACAAACACACAAATATACTATTGGTCTTTT 690
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTGCATGACTGTATACGCACACATACACAAACACACAAATATACTATTGGTCTTTT 540

Qy   691 CCTGAAGAGCCCTAATACAATATGTTATACATTTATATTGACTCTATTCAAAATTTAT 750

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Qy 8581 TAACATATTAATAATATTTGTTTATGTGTCAATATCTTAGCATGTATCAATTAAGAGACAG 8640
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Db 17531 TAACATATTAATAATATTTGTTTATGTGTCAATATCTTAGCATGTATCAATTAAGAGACAG 17590

Qy 8641 AGTCTAACGTTCTCTTTTGAAAGAGAATATAGGAATTCAGAGATATTAAGAGATTCT 8700
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Db 17591 AGTCTAACGTTCTCTTTTGAAAGAGAATATAGGAATTCAGAGATATTAAGAGATTCT 17650

Qy 8701 CCCAGGATCACAGTTAGGTAACAGAGAGCTGGATTTTAGTCCAGGTCTGTCTACAGCTCTAA 8760
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Db 17651 CCCAGGATCACAGTTAGGTAACAGAGAGCTGGATTTTAGTCCAGGTCTGTCTACAGCTCTAA 17710

Qy 8761 CGTATATACACCCTTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATC 8820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 17711 CGTATATACACCCTTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATC 17770

Qy 8821 TAAGTCAGGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAATATTTCAGGCTTGT 8880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 17771 TAAGTCAGGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAATATTTCAGGCTTGT 17830

Qy 8881 GGACCCATGGTCTCTATCATAAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAA 8940
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Db 17831 GGACCCATGGTCTCTATCATAAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAA 17890

Qy 8941 GCAAAATATAAACTAACGAATGTGGCTGTTTTATGGGATTTTTTTAACTCTTTATTTA 9000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 17891 GCAAAATATAAACTAACGAATGTGGCTGTTTTATGGGATTTTTTTAACTCTTTATTTA 17950

Qy 9001 CAAAAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTG 9060
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Db 17951 CAAAAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTG 18010

Qy 9061 AGAAAATCTTATATTTATGGACAACATTAGACTGTGACTTGCCAAGTAAGAACAAGAAG 9120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18011 AGAAAATCTTATATTTATGGACAACATTAGACTGTGACTTGCCAAGTAAGAACAAGAAG 18070

Qy 9121 CTCTGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATG 9180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18071 CTCTGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATG 18130

Qy 9181 ATAAGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAAGAATAATGACC 9240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18131 ATAAGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAAGAATAATGACC 18190

Qy 9241 ATAGACTCCTGAACAAGAAATGTCTGGACTCTGGCTTAGGCGTCCA 9300
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 18191 ATAGACTCCTGAACAAGAAATGTCTGGACTCTGGCTTAGGCGTCCA 18250

Qy 9301 GGCCAAGTTACCTAATCCTCTCCAGGCCTCCATTTTCTTATCATTAAATGAAGATAATAAA 9360
         |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db 18251 GGCCAAGTTACCTAATCCTCCCAGGCCTCCATTTTCTTATCATTAAATGAAGATAATAAA 18310

Qy 9361 AGTATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAA 9420
         |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 18311 AGTATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAA 18370

Qy 9421 TAGGGCCCAGCCTATATTAATTAATTATCAATAAAATGCCAG 9458
         ||||||||||||||||||||||||||||||||||||||||||
Db 18371 TAGGGCCCAGCCTATATTAATTAATTATCAATAAAATGCCAG 18408

RESULT 4

Qy 541 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 600
Db   CTGAAGAGGCCCTAATACAACATATGTATACATTTATATTGACTCTATTTCAAAATTTAT

Qy 751 GGTTTTGGTGAAACATATGTGGAGATGGGGCATAGGTGTGTGAACTGGATAGTGTCCTG 810
Db 601 GGTTTTGGTGAAACATATGTGGAGATGGGGCATAGGTGTGTGAACTGGATAGTGTCCTG 660

Qy 811 CTGATGAATGGGTGGGAGGCATCATTTGGGACAAGCCCAGGGCATCAGCTTATAGATATC 870
Db 661 CTGATGAATGGGTGGGAGGCATCATTTGGGACAAGCCCAGGGCATCAGCTTATAGATATC 720

Qy 871 AAGAGCTCAACAAGAGCACTTATGGCAAAACCTCCCACAAGACCTCTCAGAAGTTGAGA 930
Db 721 AAGAGCTCAACAAGAGCACTTATGGCAAAACCTCCCACAAGACCTCTCAGAAGTTGAGA 780

Qy 931 AACTGCTAAAAGTTCTTTATGCACAAGTGACATTTATGGATAAAATAGGGATTAGCAGGA 990
Db 781 AACTGCTAAAAGTTCTTTATGCACAAGTGACATTTATGGATAAAATAGGGATTAGCAGGA 840

Qy 991 TTCTTAAATACTTCGAACACTAACCTTCATTTCTACCAGGCAGTGGGGCCCCAAGTGC 1050
Db 841 TTCTTAAATACTTCGAACACTAACCTTCATTTCTACCAGGCAGTGGGGCCCCAAGTGC 900

Qy 1051 AGGGCCATAGGAAGTACAAGTCTGGGAGATACTAGGCTGCACTGTCTGTAGAGAATCTGA 1110
Db 901 AGGGCCATAGGAAGTACAAGTCTGGGAGATACTAGGCTGCACTGTCTGTAGAGAATCTGA 960

Qy 1111 AAAAATAATAGAGTCACTGAAATGCAGTTGGTATAATTATTGCCATGCATCATAAATTCT 1170
Db 961 AAAAATAATAGAGTCACTGAAATGCAGTTGGTATAATTATTGCCATGCATCATAAATTCT 1020

Qy 1171 AAATCATACTAGTGGTCAAATACTCTTCCCTGAAAAAACATTTCTTGGTTTGAATTCTA 1230
Db 1021 AAATCATACTAGTGGTCAAATACTCTTCCCTGAAAAAACATTTCTTGGTTTGAATTCTA 1080

Qy 1231 AATAATTGTTGTGGTCACCACTGAGCTTTAAATATATAAATACTTTCAAGTTTGCATAT 1290
Db 1081 AATAATTGTTGTGGTCACCACTGAGCTTTAAATATATAAATACTTTCAAGTTTGCATAT 1140

Qy 1291 TTTTATTACCTGTTCCTTAACAAACATTGAATTCAACATGAAAATGTATATGGGAAACAT 1350
Db 1141 TTTTATTACCTGTTCCTTAACAAACATTGAATTCAACATGAAAATGTATATGGGAAACAT 1200

Qy 1351 TCGGGTATACAGTCCCTGACCTCTTAAGGACTCAGGTAAATACTTAGGGTATTTCATGGCC 1410
Db 1201 TCGGGTATACAGTCCCTGACCTCTTAAGGACTCAGGTAAATACTTAGGGTATTTCATGGCC 1260

Qy 1411 CTAGTCTTTGGGGTACCACATGTTCTTCTTCAAATCACAGATTCAAGAATGAT 1470
Db 1261 CTAGTCTTTGGGGTACCACATGTTCTTCTTCAAATCACAGATTCAAGAATGAT 1320

Qy 1471 AACACAGTGATTGTGTAGACAAAATAAGTGAACCAAAATTGCTTGCTTCTTCTTCATTCTAT 1530
Db 1321 AACACAGTGATTGTGTAGACAAAATAAGTGAACCAAAATTGCTTGCTTCTTCTTCATTCTAT 1380

Qy 1531 GGAACCACTGAGAGTTTTACTTGTGCTTAAAATTTGAATAGTAAAACAGAGTGTCAAC 1590
Db 1381 GGAACCACTGAGAGTTTTACTTGTGCTTAAAATTTGAATAGTAAAACAGAGTGTCAAC 1440

Qy 1591 TTCATGCTGGAATATTTTGGCTTTTAGACACAATTTAAGTACATGAAGTATTTTTAC 1650
Db 1441 TTCATGCTGGAATATTTTGGCTTTTAGACACAATTTAAGTACATGAAGTATTTTTAC 1500

Qy 1651 AAGACTAAGTAACATCACTGAAATTACAGCCTTCTTCTTTAAAACTGGTATTTGTTAT 1710
Db 1501 AAGACTAAGTAACATCACTGAAATTACAGCTTTCTTCTTTTAAAACTGGTATTTGTTAT 1560

Qy 1711 AAAACTAAAGAGCGAATCAAGAAAAGCATAATATTATTACTGATTATTACAGGATTATTACT 1770
Db 1561 AAAACTAAAGAGCGAATCAAGAAAAGCATAATTATTACTGATTATTACAGGATTATTACT 1620

Qy 1771 GAAAAAGAAATGTACGGAATAGAGGAGGAGGAGTTAACAAATGATCCACTCTGGGTGT 1830
Db 1621 GAAAAAGAAATGTACGGAATAGAGGAGGAGGAGTTAACAAATGATCCACTCTGGGTGT 1680

Qy 1831 GAAAACACCAATAAGCCTGCTTCCAGGAAGTGCCTAAGACAGAGCTGGCTCAGCTTGCTG 1890
Db 1681 GAAAACACCAATAAGCCTGCTTCCAGGAAGTGCCTAAGACAGAGCTGGCTCAGCTTGCTG 1740

Qy 1891 GGTCACAGCATGTAAGGAAACTGCTGGGCTACAATGCCACCATCCTCAGTTGTCCAGATAG 1950
Db 1741 GGTCACAGCATGTAAGGAAACTGCTGGGCTACAATGCCACCATCCTCAGTTGTCCAGATAG 1800

Qy 1951 ATAATCCCATAGCCCCATGGGGGAAATAATCTTTAATTATGATATAGCTGACACCATTCAA 2010
Db 1801 ATAATCCCATAGCCCCATGGGGGAAATAATCTTTAATTATGATATAGCTGACACCATTCAA 1860

Qy 2011 AGCACTATGCTAAGTCCTTATGTGAATTAACTTTGTCAAATTAATTTATTTTCATAAATAA 2070
Db 1861 AGCACTATGCTAAGTCCTTATGTGAATTAACTTTGTCAAATTAATTTATTTTCATAAATAA 1920

Qy 2071 CCCAAATATGTATACCACTATTATCCTACCTTAAAGAGGAGAAACTGAGCTCCTAAAGT 2130
Db 1921 CCCAAATATGTATACCACTATTATCCTACCTTAAAGAGGAGAAACTGAGCTCCTAAAGT 1980

Qy 2131 TAAATATCTAACCCAAGTTAAGACTGCTAGTCACCCTAGGCTATTAACTCAGGCAGTCTA 2190
Db 1981 TAAATATCTAACCCAAGTTAAGACTGCTAGTCACCCTAGGCTATTAACTCAGGCAGTCTA 2040

Qy 2191 ACTCAGGTATAATAACATTATGCTACTACTGTTGCAGCTTGACTATGCCTGAATTATAACG 2250
Db 2041 ACTCAGGTATAATAACATTATGCTACTACTGTTGCAGCTTGACTATGCCTGAATTATAACG 2100

Qy 2251 TCATGCTATCTCAACTAAAAAGCTAAGGGAAATAAAATGAGCCATAGGGCTCAATTTCATA 2310
Db 2101 TCATGCTATCTCAACTAAAAAGCTAAGGGAAATAAAATGAGCCATAGGGCTCAATTTCATA 2160

Qy 2311 AAAGGAGAGAAAATACTGGGGAAAAGTGATAATGCAGAGTTAAAATATTTTGTAAAAG 2370
Db 2161 AAAGGAGAGAAAATACTGGGGAAAAGTGATAATGCAGAGTTAAAATATTTTGTAAAAG 2220

Qy 2371 TGCCAGAGATTGAGTATAACAAGTGTGACCAAAAAAAAAAAAAAAAAAGGAAGA 2430
Db 2221 TGCCAGAGATTGAGTATAACAAGTGTGACCAAAAAAAAAAAAAAAAAAGGAAGA 2280

Qy 2431 AGGTAAAAAAAGAGAGGGAGGTCTGAGAAATAGAAATCAGAGGAAGGAAATAAAGGAGG 2490
Db 2281 AGGTAAAAAAAGAGAGGGAGGTCTGAGAAATAGAAATCAGAGGAAGGAAATAAAGGAGG 2340

Qy 2491 GTGAGAGTAAATTCTTTAGCATTCATTGACCTAACATTTCATTGCAGTTAGCTAAAGGA 2550
Db 2341 GTGAGAGTAAATTCTTTAGCATTCATTGACCTAACATTTCATTGCAGTTAGCTAAAGGA 2400

Qy 2551 TTTTACCAACTAAGGAAAAATAACACTTGACCTAACATTTCATTGCAGTTAGCTAAAGGA 2610
Db 2401 TTTTACCAACTAAGGAAAAATAACACTTGACCTAACATTTCATTGCAGTTAGCTAAAGGA 2460

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                                          10535500-11_vs_10535500a11na.txt

Db  3361  TGGTAATGTAAAACAAACTCAGTACAGTAGTATTCAGTACAGTATTTAAGCCCCTGTACT  3420

Qy  3571  TAAACATATTCCTCGTACCAATGAAGTACATGAAAAGCAAATTGTGTGAGATATCGTA    3630
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  TAAACATATTCCTCGTACCAATGAAGTACATGAAAAGCAAATTGTGTGAGATATCGTA    3480

Qy  3631  GATGGAAGTAAATTAGTCTTTATGTCCCCACAAATTGAAATGCATTCAAAAACTCTGT    3690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  GATGGAAGTAAATTAGTCTTTATGTCCCCACAAATTGAAATGCATTCAAAAACTCTGT    3540

Qy  3691  GTGTGTATGTGTGTGTGTGCAGAGTGTGTGTGAGAGGACACAGAGGATACGGCTTTGG    3750
          ||||||||||||||||||||| ||||||||||| ||||| ||||||||||||||||
Db  3541  GTGTGTATGTGTGTGTGTGTGACAGAGTGTGTGTGAGAGAGCAGAGGATACGGCTTTGG   3600

Qy  3751  TTGCCTCCATAAGCTGGCTGCTATGATGATTAATAAGACCAAGTTTCTAAAGAAAATGAGAT 3810
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  TTGCCTCCATAAGCTGGCTGCTATGATGATTAATAAGACCAAGTTTCTAAAGAAAATGAGAT 3660

Qy  3811  CATAACAAAAGCCCTCTTTATGACTATCTTTATCAGGGGCAAAAAGGAAAAGAGACAAAA   3870
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db  3661  CATAACAAAAGCCCTCTTTATGACTATCTTTATCAGGGGCAAAAAGGAAAGAGACAAAA    3720

Qy  3871  CAGCATGAAATGATGAGCAGCCTGTTACTATGATGAAAATTCATCACAATGATTGCTTTCAAGAGT 3930
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  3721  CAGCATGAAATGATGAGCAGCCTGTTATCCTGATGAAAATTCATCACAATGATTGCTTTCAAGAGT 3780

Qy  3931  AATTTCTCTGGGTAATTCAGCAGCCCGTGTTACTATGGCTCTCTGGAGTGATAGCTAATGT 3990
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  AATTTCTCTGGGTAATTCAGCAGCCCGTGTTACTATGGCTCTCTGGAGTGATAGCTAATGT 3840

Qy  3991  AAATGAAGCCTCTAAAAGTGGATTATCCTGACAAGAATATACTCAGCCAATAATGCAACA  4050
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  AAATGAAGCCTCTAAAAGTGGATTATCCTGACAAGAATATACTCAGCCAATAATGCAACA  3900

Qy  4051  GAAATCCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAAATATTTT            4110
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  GAAATCCATTCAAAGCATTCGGGAAAAATTCAAAAGAATAAAATATTTTTTT         3960

Qy  4111  AAAGTTAATGACCTAGCATCCATTCTTCCCGACTAACAGCAGCAAGCACTTAAAAAT     4170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  AAAGTTAATGACCTAGCATCCATTCTTCCCGACTAACAGCAGCAAGCACTTAAAAAT     4020

Qy  4171  ATCCAGCCAGGATGAAATAGAAACCCACCTGACTTGTAATATTTTTGGTCCCAGG      4230
          ||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  4021  ATCCAGCCAGGATGAAATAGAAACCCACCTGACTTGTAATATTTTTGTTGGTCCCAGG    4080

Qy  4231  GACTCAGATTCTAAGCCAAATTCTTGAATGATCTTGGCAAATGTCTCGGAATTATTTTG   4290
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081  GACTCAGATTCTAAGCCAAATTCTTGAATGATCTTGGCAAATGTCTCGGAATTATTTTG   4140

Qy  4291  CCAACTTTCTTTATCTTGGAAAAAAAGTTCATGAATGGGTGTCAAATTGATTAGTT     4350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141  CCAACTTTCTTTATCTTGGAAAAAAAGTTTCATGAATGGGTGTCAAATTGATTAGTT     4200

Qy  4351  TAAAACCTTTTGCAGATGTGGCACCCTAAAACTGTATTAGAAAAAAAGTAAGT        4410
          |||||||||||||||||||||||||||||||||||||||||||||||||||||-------
Db  4201  TAAAAACCTTTTGCAGATACGTATGGCACCCTAAAACTGTATTAGAAAAAAA          4254

Qy  4411  ACTCTGTAGTGTGAAAAATTCTTAAAGGACACCGCACCCTCTTTACAAACTCACAAAAACAGCC 4470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4255  ------------------------------------------------------------    4254

Qy  4471  TTTGGAATACCCACATGAAGTAGCTGTTGTTATTGCTTTCTATATACCTACATCTTGTCT   4530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                      Page 38


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Qy  2611  TGCTAGAAAACTATGTTGCAGTGGTTGCTCTAATTCTTCAGGAATAGAGAAAAGTGA      2670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  TGCTAGAAAACTATGTTGCAGTGGTTGCTCTAATTCTTCAGGAATAGAGAAAAGTGA      2520

Qy  2671  CAAAAGATCAGAGAAGAAGGAAACTATCAGAAAAATACAGAATTGGAGTAGGA          2730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CAAAAGATCAGAGAAGAAGGAAACTATCAGAAAAATACAGAATTGGAGTAGGA          2580

Qy  2731  TATAACATATTTGGGTGAAGGTAAAATTTATATTGTAATCTTAAGTATCTTGCTACTT     2790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  TATAACATATTTGGGTGAAGGTAAAATTTATATTGTAATCTTAAGTATCTTGCTACTT     2640

Qy  2791  CAGTTTGGTCCCTGGAACAGCAGCATCAGAATCTGCCGCAGGGCTTGTTAAAAGGCAGAA   2850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  CAGTTTGGTCCCTGGAACAGCAGCATCAGAATCTGCCGCAGGGCTTGTTAAAAGGCAGAA   2700

Qy  2851  TCTCAGGTCCATCCCAGACTCACTGAATCAGAATATAAATACTGACAAGATGCCCCGGG   2910
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  2701  TCTCAGGTCCATCCCAGACTCACTGAATCAGAATATAAATACTGACAAGATGCCCCGGG   2760

Qy  2911  ATCATATGCACAGTAGAGCTGGCGAAGTTCCATTGTCCATTGTTTTCTGCAAC          2970
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  2761  ATTCATATGCACAGTAGAGCTGGCGAAGTTCCATTGTCCATTGTTTTCTGCAAC         2820

Qy  2971  TTAGTATTTCTGAGTTTTCCCAAGGAAGAAAACCCAGGCCTTAGCTTCTGGCAGACTTGT   3030
          |||||| |||||||||||||||||||||||||||||||||||||||||||||| |||
Db  2821  TTAGTATTTCTGAGTTTTCCCAAGGAAGAAAACCCAGGCCTTAGCTTCTGGCAGACTTGT   2880

Qy  3031  GTTCTCCTTACTTACTAGCTGCATGCATGAGGCAAGGAAATCAAACTTTATGTGCC       3090
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  GTTCTCCTTACTTACTAGCTGCATGCATGAGGCAAGGAAATCAAACTTTATGTGCC       2940

Qy  3091  TCAGTTTCCTCATCTATAAAATGGAGACTATAATAATCATCTCCTAGGCTTGTTTTGAGG   3150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db  2941  TCAGTTTCCTCATCTATAAAATGGAGACTATAATAATCATCTCCTAGGCTTGTTTTGAGG   3000

Qy  3151  ATGTTCAACAAATGCTCCTTTCATTCCTCTATTACAGACCTGCCGGAGCAAATTCTGCT    3210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  ATGTTCAACAAATGCTCCTTTCATTCCTCTATTACAGACCTGCCGGAGCAAATTCTGCT    3060

Qy  3211  AGCAGCCTTTGTGTCATTATCTGTTTCTAAACTTAGTAATTGAGTCTGGAGACT        3270
          |||||||||||||| ||||||||||||||||||||||||||||||| |||||||
Db  3061  AGCAGCCTTTGTGTCTATTATCTGTTTCTAAACTTAGTAATTGAGTGTGATCTGGAGACT   3120

Qy  3271  AACTCTGAAATAAATAAGCTGATTATTTATTTCTCAAAACAACAGAATACCGATTT      3330
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  3121  AACTCTGAAATAAATAAGCTGATTATTTAATTTATTTCTCAAAACAACAGAATACCGATTT  3180

Qy  3331  AGCAAATTACTTCTTAAGATATATTTTACATTCTATATTCTCTACCCTGAGTTGATG     3390
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  AGCAAATTACTTCTTAAGATATTTTTTACATTCTATATTCTCTACCCTGAGTTGATG     3240

Qy  3391  TGTGAGCAATATGTCACTTCATAAAGCCAGGTATACATTATGGACAGGTAAGTAAAAAA   3450
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  TGTGAGCAATATGTCACTTCATAAAGCCAGGTATACATTATGGACAGGTAAGTAAAAAA   3300

Qy  3451  CATATTATTATTCTACGTTTTTGTCCAAAAATTTAAATTTGCGCGGTGTGT          3510
          |||||||||||||||||||| ||||||||||||||||||||||| ||||||
Db  3301  CATATTATTATTCTACGTTTTTGTCCAAAAATTTAAATTTCAACTGTTGCGCGGTGTGT   3360

Qy  3511  TGGTAATGTAAAACAAACTCAGTACAGTAGTATTCAGTACAGTATTTAAGCCCCTGTACT  3570
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                                                                      Page 37
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Qy 5431 TAACTCATTCTCACTTCTTATTCCATGATGAAATGACATAAATGACAGGTTTTTTATTGTTG 5490
Db 4255 -- 4254
Qy 5491 TTGTTGTTGTTTTCTGGACACAAGGCAAGGTAGCTACCTGGGCAGAGAGCTGTGTTTATTTCT 5550
Db 4255 -- 4254
Qy 5551 CTATGCCGTGGAGGAGAAATTGGTTAATTGGCCATGGAAGGCAGTCATTAAGATGTTCCCA 5610
Db 4255 -- 4254
Qy 5611 TGCGAGTGAACTTTCCAGGGTTCCAGCTTCTGCATCCTTCCCGTCCCTCAATTCATT 5670
Db 4255 -- 4254
Qy 5671 GTTGGTGATGACAATGTCTCTCCCATCAGCCTCATGAAGTCTCTCATTTATTTAAAAT 5730
Db 4255 -- 4254
Qy 5731 TTGCTTCAGGAAAAATTTGAAAATGTCCAGTAATGCCTGATTGGCCCCTTATCCTA 5790
Db 4255 -- 4254
Qy 5791 AAGGCTTAAACTGGAGGAAGGAAGCTAAACTGAGAAATCTTGCAAATCATTGAGCCAAAA 5850
Db 4255 -- 4254
Qy 5851 ACGTATTAATAGCAAGATCTATCATTTATTGACTAGTATGTGGCAGGCAGTGCCCTTTTA 5910
Db 4255 -- 4254
Qy 5911 TTTAGGCAGGAGAGTTGATGGGGGGGCGGGGGTTCACACATCTTAAAGAGGTGCTATCT 5970
Db 4255 -- 4254
Qy 5971 CCTCCTATATAAATCATGTAAGTCAAGAGAGTAAGGAATTGTCTTTGTTTGGTTATATTC 6030
Db 4255 -- 4254
Qy 6031 AGGGGATTAGAGTATACAGTAGAAGATCCCAAGAAACCTTGGGATCATTTAGACTAAGA 6090
Db 4255 -- 4254
Qy 6091 AATGCCAATACCGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGAGAGGCCG 6150
Db 4255 -- 4254
Qy 6151 AGGTGGGCGGATCACAAGGTCAGGAGATTGAGACCGTCCTGGCTAACGTGGTGAAACCCT 6210
Db 4255 -- 4254
Qy 6211 GTCTCTACTAAAAATACAAAAAATTAGCCGGGCGGTGGTGCGGGCGCCTGTAGTCCCAGC 6270
Db 4255 -- 4254
Qy 6271 TACTCGGAGGGGCGGAGGCAGGAGAATGGTGTGAACTCAGGAGGCGGAGCTTGCAGTCAGC 6330
Db 4255 -- 4254
Qy 6331 CGAGATTGCCCCAATGCACTCCAGCCTGGGCGACAAGAACGACTCCGTCTCAGAACAAA 6390
Db 4255 -- 4254

10535500-11_vs_10535500a11na.txt

Db 4255 -- 4254
Qy 4531 ATTATAAAAAGACTGGTTTTGGCAGGTGGTGGTGCACACCTGTAATTCCAGCACTTT 4590
Db 4255 -- 4254
Qy 4591 GGGAGGCCAAGGCGGGCGGGGCGGGATCGAGATCAGGAGGTTCAGGACCAGCCTGATCAATAT 4650
Db 4255 -- 4254
Qy 4651 GGTGAAACCCAGTCTTTACTGAAAATACAAAAATCACCCGGGTGGTGGTGACGGGGCGCCTG 4710
Db 4255 -- 4254
Qy 4711 TAGTCCCAGCTACTCGGGTAGCTGAGGCAGGAGAATCACTTGAACTCAGGAGTCAGAGGT 4770
Db 4255 -- 4254
Qy 4771 TGCAGTGAGCTGAGATCATGCCACTGCCACTCCAGCCTGGGTGACAGAGCAAGACTCCATC 4830
Db 4255 -- 4254
Qy 4831 TCAAAAAAAAAAAAAAGACTGGTTTTTCAACAGCTATTCCCACCCCTCTGCATGGA 4890
Db 4255 -- 4254
Qy 4891 AATATTCACCCAGTCAATTGTTTCCTAGTTTGGGTAATGCCCTCTGGGCAGGACTGGA 4950
Db 4255 -- 4254
Qy 4951 GTGGGGCACACAGGAGGAGAAGCTGCAAACTATGTTTAGAAGCATGTCTGGGAAATGTCATGC 5010
Db 4255 -- 4254
Qy 5011 AAGAAAAGACATATTTAAAGGTAGGCTTGCATGAATGGAAAAGGAGAGTAATTCTATGT 5070
Db 4255 -- 4254
Qy 5071 AGAGCAGAGCCTCTACTTGCAGTGAGGAAGAGCAAAAGTGGGGAAGGCAAGAGGAATTATG 5130
Db 4255 -- 4254
Qy 5131 CTTTTCATCAGCCAAATTTGCAGGTAGGAGGATTGGCTCAGTCATCTTGGCTGAGCTCA 5190
Db 4255 -- 4254
Qy 5191 TGAAACCAGGTGTAAAGAAAGTGGACTAGATTCATCCATTACAGGGAAGAGGAGAGCC 5250
Db 4255 -- 4254
Qy 5251 GTGAAAGATAATCCAGAAATCATTGGGGATTTGATGGTAGAAGGTATTTTGGGACTATTCC 5310
Db 4255 -- 4254
Qy 5311 ATTTGAAATGAGAAGGTACCTGACATTCTTTGAATTCCTTTCAAGCAAAGGATTAAATTT 5370
Db 4255 -- 4254
Qy 5371 ACCCATGAGTTGACTCAGAAAAACATAAAAAGTATTGTTGCTGCTGCTCTCAGAGTTTTATC 5430
Db 4255 -- 4254

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10535500-11_vs_10535500allna.txt

Qy  6391  ACAAAAGGAAATGCCAATACCAGCAGAAATAGACCAAATCATGAACATAAGCTAAACAA  6450
Db                                                                  4254
Qy  6451  ATGTTGGCAGTGTAGCCTAGTGTGGTTAAGAGAGCAGACTCTTAACTAGAACACTGCACTCC  6510
Db                                                                  4254
Qy  6511  ATGTCCTCACTGTAGACCCTCACTGTGGGGTTCTAATTAACCCCTGTTACTTACCAGTGG  6570
Db                                                                  4254
Qy  6571  CAGTCTTAAGGCATTCCTTAAGTTCGGTTGTGCCCCAATTTGTTCATCTGTAGAAGGGGTA  6630
Db                                                                  4254
Qy  6631  GGATGACAGTAGTGTTTACTTTATAGGCTTACTGTGAGCATTAAATGAGTTACTACTGTA  6690
Db                                                                  4254
Qy  6691  TTTGTAAAGTGCTTAAAAATGCTGCTCCAAAAGAGTTTGTTAAACACTTAAGGAACTGATTT  6750
Db                                                                  4254
Qy  6751  ACTTGCATCTAAACTGACAGCTCTCAATAACTGGAAATGATCAAGCATAGGCCCTGGAAT  6810
Db                                                                  4254
Qy  6811  ATAAGCAGGTCTACATGCAAAATGTTCGTTCTTTTGTTCAGCCCTGTGCCTAGA  6870
Db                                                                  4254
Qy  6871  TCAATATCTAGTGATCATGCTCAAGAGAATATTGTTGAATGAATCAATGAACCTACCGAGG  6930
Db                                                                  4254
Qy  6931  TAGTTACTACATAAAAGAGTTCTGCATGAGTACAAATCTGGGCAAAGTGACCTCCAAGGAAAT  6990
Db                                                                  4254
Qy  6991  TTCCACTTTTAGATTCGTGTGATTTCCTTAAGGAACTGATAAATTGGTGTGATACAATGTA  7050
Db                                                                  4254
Qy  7051  AAAAAATGTGCCTATATGATTTGAGAAAAACTTATTTCTCTCCCTCTTTTTTCCTTCCT  7110
Db                                                                  4254
Qy  7111  TCCTTCCTCCCTCCCTTCCTCCCTCCCTCCCTCCCTCCCTCCCTTCCTCCCTCCCTCCT  7170
Db                                                                  4254
Qy  7171  TCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC  7230
Db                                                                  4254
Qy  7231  TTTCTTCTTCTCTTCTTCTTCTTCCTTCTTCTTTGTGCCTTTCTTTCTTTCTTTCTTTCT  7290
Db                                                                  4254
Qy  7291  TTCTTCTTCTGTCCTTCTTTCTTCTTTCTTCCTTCTTCTTCTTCTTGCCTTTCTTTCTTGT  7350

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10535500-11_vs_10535500allna.txt

Db                                                                  4254
Qy  7351  TTTCTTCTTCCTTCTTTTTCCTTAAGCAGACCATGTCTGTTAGATGAATGCCTTT  7410
Db                                                                  4254
Qy  7411  TTCTAGTTAAAAGGTTAAACAGGAAAGTGAAGCACAATTATCAAGGGTCTCCAGTCATCT  7470
Db                                                                  4254
Qy  7471  CCACATGTTCTTAATCATTATCTCTTTACAGTTCATATCTCCAGGCCTTCATTGGG  7530
Db  4255  ------------------------TTTCATATCTCCAGGCCTTCATTGGG  4281
Qy  7531  TCAGGTTGGCATTTCGCTGCCCTTATGTGTGTGACAAGTGAAAATAAGGAAAGAAAAAA  7590
Db  4282  TCAGGTTGGCATTTCGCTGCCCTTATGTGTGTGACAAGTGAAAATAAGGAAAGAAAAAA  4341
Qy  7591  ACTCAAGTGAAGAAAATCAGAATCTGCGCAGCAGTTCCTGGGCGGTTCAGCTGCTTCCCA  7650
Db  4342  ACTCAAGTGAAGAAAATCAGAATCTGCGCAGCAGTTCCTGGGCGGTTCAGCTGCTTCCCA  4401
Qy  7651  CATCACCTGCCTCATCAAGCCCCAGCATCCATCCTGCTCATCTTACACCCTGTGTGC  7710
Db  4402  CATCACCTGCCTCATCAAGCCCCAGCATCCATCCTGCTCATCTTACACCCTGTGTGC  4461
Qy  7711  ATGACAGGCCCACCATTCATTTATCAGAGCAAAGGCTCTCCCACTATTCTGGTTCACCCC  7770
Db  4462  ATGACAGGCCCACCATTCATTTATCAGAGCAAAGGCTCTCCCACTATTCTGGTTCACCCC  4521
Qy  7771  CCTACTTAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCTGGGAGCTCA  7830
Db  4522  CCTACTTAGCCAGATATACAAGAATATCTGCACGGATGACCTGCCTCACCTGGGAGCTCA  4581
Qy  7831  GAGGAGCTCAGATTCCATTACTACTATCGGCACCAAGGACAGATCTCCCAGCAAGAATGACAGA  7890
Db  4582  GAGGAGCTCAGATTCCATTACTACTATCGGCACCAAGGACAGATCTCCCAGCAAGAATGACAGA  4641
Qy  7891  AAAGACTAACTGCCCCAAAATCTCCCTCCAAAACACAGTTCTCTAATTCTCCCAAGA  7950
Db  4642  AAAGACTAACTGCCCCAAAATCTCCCTCCAAAACACAGTTCTTAATTCTCCCAAGA  4701
Qy  7951  AACCAGAATGTGACTGCTCACCTCTCAAGGACCTGAAAACAACTGGCCATTCAGCTAT  8010
Db  4702  AACCAGAATGTGACTGCTCACCTCTCAAGGACCTGAAAACAACTGGCCATTCAGCTAT  4761
Qy  8011  TTAAATCAACTTAAAAAAATCCAACCGCCAAAATATTAAACCATTTTGGTTGGAATGATA  8070
Db  4762  TTAAATCAACTTAAAAAAATCCAACCGCCAAAATATTAAACCATTTTGGTTGGAATGATA  4821
Qy  8071  ACATAACTAACCTGCTGACAGCGTTGCTTCTGCTAGGTGCAAAAATGGAAAAAAATACTT  8130
Db  4822  ACATAACTAACCTGCTGACAGCGTTGCTTCTGCTAGGTGCAAAAATGGAAAAAAATACTT  4881
Qy  8131  CTAATCAGGTCAAATCACTCTACCTTTGGGATTCTAAATTTACTCATATTCTCAAAGAAA  8190
Db  4882  CTAATCAGGTCAAATCACTCTACCTTTGGGATTCTAAATTTACTCATATTCTCAAAGAAA  4941
Qy  8191  TATATTCAGTCATAGTGGGGAAAATAGGATTATTCCTTTAGCTCGATAAGCAACCAGAAG  8250
Db  4942  TATATTCAGTCATAGTGGGGAAAATAGGATTATTCCTTTAGCTCGATAAGCAACCAGAAG  5001
Qy  8251  TTCTTCCTTCAAATCTTGACATTTAATCAATCAGAAATTGATTTTTGGAAAACTGTTTCC  8310

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Qy  9211  CAGTTATAAGGAGCACAAAGAATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTT  9270
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Db  5962  CAGTTATAAGGAGCACAAAGAATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTT  6021

Qy  9271  CTGGCTTAGGCACTCCTTGTGTATGGTCCAGGCCAAGTTACCTAATCTCTCCAGGCCTCC  9330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6022  CTGGCTTAGGCACTCCTTGTGTATGGTCCAGGCCAAGTTACCTAATCTCTCCAGGCCTCC  6081

Qy  9331  ATTTTCTTATCATTAAATGAAGATAATAAAAGTATTTTCCTCAGAGAGCTGTAAGAATAA  9390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6082  ATTTTCTTATCATTAAATGAAGATAATAAAAGTATTTTCCTCAGAGAGCTGTAAGAATAA  6141

Qy  9391  ACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCAGCCTATATTAATTTATCAATA  9450
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6142  ACTGAGCTAACCCATGTCAAGCACATAGAATAGGGCCCAGCCTATATTAATTTATCAATA  6201

Qy  9451  AATGCCAG  9458
          ||||||||
Db  6202  AATGCCAG  6209
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RESULT 5
US-10-535-500A-2

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; Sequence 2, Application US/10535500A
; GENERAL INFORMATION:
;   APPLICANT: Rigshospitalet
;   APPLICANT: Henrik Leffers
;   APPLICANT: Anne Mette Buhl Hertz
;   APPLICANT: Jorgen Kjems
;   TITLE OF INVENTION: Methods and kits for diagnosing and
;   TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
;   FILE REFERENCE: P34546US01
;   CURRENT APPLICATION NUMBER: US/10/535,500A
;   CURRENT FILING DATE: 2005-05-18
;   PRIOR APPLICATION NUMBER: DK/PA 200201792
;   PRIOR FILING DATE: 2002-11-19
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 3893
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-535-500A-2
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  Query Match             24.7%;  Score 2333.5;  DB 1;  Length 3893;
  Best Local Similarity   55.7%;  Pred. No. 1.5e-20;
  Matches 3893;  Conservative   0;  Mismatches   0;  Indels 3099;  Gaps   1;
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Qy  2467  ATCAGAGGAAGGAAATAAAGGAGGGTGAGAGTAAATTCTCTTTAGCATTCAGATTCCAC  2526
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATCAGAGGAAGGAAATAAAGGAGGGTGAGAGTAAATTCTCTTTAGCATTCAGATTCCAC  60

Qy  2527  AGATTCCACAATCACATTTCTTTTTACCAACTAAGGAAAAATAACACTTGACCTAAC  2586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AGATTCCACAATCACATTTCTTTTTACCAACTAAGGAAAAATAACACTTGACCTAAC  120

Qy  2587  ATTTCATTGCAGTTAGCTAAAGGATGCTAGAAAAAGATCAGAGAAGAAGAAACTATCA  2646
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  ATTTCATTGCAGTTAGCTAAAGGATGCTAGAAAAAGATCAGAGAAGAAGAAACTATCA  180

Qy  2647  TTCTTCAGGAATAGAGAAAAGTGACAAAAAGTGAGAGAGAGAAGGAAAGGAAACTATCA  2706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TTCTTCAGGAATAGAGAAAAGTGACAAAAAGTGAGAGAGAGAAGGAAAGGAAACTATCA  240
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Db  5002  TTCTTCCTTCAAATCTTGACATTTAATCAATCAGAAATTGATTTTGGAAAACTGTTCC  5061
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy  8311  TATGAAGCTATCTGCCTGAAGGATTTCTTTACAATCCAGACTATAGAAGGAAAT  8370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5062  TATGAAGCTATCTGCCTGAAGGATTTCTTTACAATCCAGACTATAGAAGGAAAT  5121

Qy  8371  CACAACCTGGACTTCACCTCCATTGGTCAGAGTTTACTGACCAATTCCCACCTCGCC  8430
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5122  CACAACCTGGACTTCACCTCCATTGGTCAGAGTTTACTGACCAATTCCCACCTCGCC  5181

Qy  8431  TACACCTAACGGAAGTTATGCCTGTTTCTCTCACATACCCCAACAGTTACAAATGG  8490
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5182  TACACCTAACGGAAGTTATGCCTGTTTCTCTCACATACCCCAACAGTTACAAATGG  5241

Qy  8491  TGTTATTATTAAGCATCTTTATTTTGTGGCCTCTGATTACATGGTCCCCTAAATTTTG  8550
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5242  TTGTATTATTAAGGATCTTTATTTTGTGGCCTCTGATTACATGGTCCCCTAAATTTTG  5301

Qy  8551  ACCTAATCACAAAAGATTGGTAAAATTTCTTAAACATATTAATAATATATTTGTTTATGTGT  8610
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5302  ACCTAATCACAAAAGATTGGTAAAATTTCTTAAACATATTAATAATATATTTGTTTATGTGT  5361

Qy  8611  CAATATCTTAGCATGTATCAATTAAGACAGAGGTCTTAACGTTCTCTTTTTGAAAGAGAA  8670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5362  CAATATCTTAGCATGTATCAATTAAGACAGAGGTCTTAACGTTCTCTTTTTGAAAGAGAA  5421

Qy  8671  TATTAGGATTCAGAGATATTAAGAGATTCTCCCAGGATCACAGTTAGGTAACAGAGCTGG  8730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5422  TATTAGGATTCAGAGATATTAAGAGATTCTCCCAGGATCACAGTTAGGTAACAGAGCTGG  5481

Qy  8731  ATTTTAGTCCAGGTCTGTCTACAGCTCTAAGCTACTATATACACCCTTGTATAACATGTCAC  8790
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5482  ATTTTAGTCCAGGTCTGTCTACAGCTCTAAGCTACTATATACACCCTTGTATAACATGTCAC  5541

Qy  8791  GAATTCAGGATAAAGGGATCTTCAGTGATCTAAGTCAGGGGTCAGCAACCTTTTCTAAA  8850
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5542  GAATTCAGGATAAAGGGATCTTCAGTGATCTAAGTCAGGGGTCAGCAACCTTTTCTAAA  5601

Qy  8851  AGGACCAAATAGTAATATTTCAGGCTTTGTGGACCCTATGGTCTCTATCATAACTGTTCA  8910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5602  AGGACCAAATAGTAATATTTCAGGCTTTGTGGACCCTATGGTCTCTATCATAACTGTTCA  5661

Qy  8911  AATCACCATGTAGTGTAAAAGGAGCCATAAGGCAAAATATAAACTAACGAATGTGGCTGTT  8970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5662  AATCACCATGTAGTGTAAAAGGAGCCATAAGGCAAAATATAAACTAACGAATGTGGCTGTT  5721

Qy  8971  TTATGGGATTTTTTTAACTCTTTATTTACAAAAGCAGGTGGCAGATCAGAACTCACTT  9030
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5722  TTATGGGATTTTTTTAACTCTTTATTTACAAAAGCAGGTGGCAGATCAGAACTCACTT  5781

Qy  9031  ATGGGCCATAGTTCTCTGACCCCTGACCTGAGAAAATCTTATATTTATGGACAACATTTA  9090
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5782  ATGGGCCATAGTTCTCTGACCCCTGACCTGAGAAAATCTTATATTTATGGACAACATTTA  5841

Qy  9091  GACTGTGCACTTGCCAAGTAAGACAAGAAGCTCTGTCAACTGAAGGTCAAGGCTGGAGTT  9150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5842  GACTGTGACTTGCCAAGTAAGACAAGAAGCTCTGTCAACTGAAGGTCAAGGCTGGAGTT  5901

Qy  9151  CTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAATAGTTAAAGTTAGAAGATCC  9210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5902  CTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGTGAAAATAGTTAAAGTTAGAAGATCC  5961
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Qy  2707  GAAAAATACAGAATTGGAGTAGGATAACATATTTGGGTTGAAGGTAAAATTTTATATT  2766
          ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db   241  GAAAAATACAGAATTGGAGTAGGATATAACATATTTGGGTTGAAGGTAAAATTTTATATT  300

Qy  2767  GTAATCTTAAGTATCTTGCTACTTGCAGTTGGTCCCTGGAACGCAGCATCGAATCTGC  2826
          |||||||||||||||||||||||||||||||||||||||||||   ||||||  ||||||
Db   301  GTAATCTTAAGTATCTTGCTACTTGCAGTTGGTCCCTGGAACAGCAGCATCAGAATCTGC  360

Qy  2827  CGAGGGCCTTGTTAAAAAGGCAGAATCTCAGGTCCCAGACTCACTGAATCAGAATA  2885
          ||||||||||||||||||||||||||||||||||||     |||||||||||||||||
Db   361  CGAGGGCCTTGTTAAAAAGGCAGAATCTCAGGTCCCATCCCAGACTCACTGAATCAGAATA  420

Qy  2887  TAAATACTGACAAGATGCCCCGGGATTCATATGCACAGTAGAGCTGGCGAAGTTCCATTG  2946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  TAAATACTGACAAGATGCCCCGGGATTCATATGCACAGTAGAGCTGGCGAAGTTCCATTG  480

Qy  2947  TAGCCGTGTGATTGTTTCTGCAACTTAGTATTTCTGAGTTTCCCAAGGAAGAAAACCCA  3006
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db   481  TAGCCGTGTGATTGTTTCTGCAACTTAGTATTCTGAGTTTCCCAAGGAAGAAAACCCA  540

Qy  3007  GGCCTTAGCTTCTGGCAGACTTGTGTTTCCTTACTTACTAGCTGCATGACTCATGAG  3066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGCCTTAGCTTCTGGCAGACTTGTGTTTCCTTACTTACTAGCTGCATGACTCATGAG  600

Qy  3067  CAAGGAAATCAAACTTATGTGCCTGAGTTCCTCATCTATAAATGGAGACTATAATAA  3126
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   601  CAAGGAAATCAAACTTATGTGCCTGAGTTCCTCATCTATAAAATGGAGACTATAATAA  660

Qy  3127  TCATCTCCTAGGCTGTTGTTGAGGATGTCAACAAATGCTCCTTCATTCTCCTATTTAC  3186
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   661  TCATCTCCTAGGCTGTTGTTTGAGGATGTCAACAAATGCTCCTTCATTCTCCTATTTAC  720

Qy  3187  AGACCTGCCGCAGACAATTCTGCTAGCAGCCTTGTGCTATTATCTGTTTCTAAACTTA  3246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AGACCTGCCGCAGACAATTCTGCTAGCAGCCTTGTGCTATTATCTGTTTCTAAACTTA  780

Qy  3247  GTAATTGAGTGTGATCTGGAGACTAACTCTGAAATAAATAAGCTGATTATTTATTT  3306
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  GTAATTGAGTGTGATCTGGAGACTAACTCTGAAATAAATAAGCTGATTATTTATTT  840

Qy  3307  TCTCAAAACAACAGAATACGATTTAGCAAATTACTTCTTAAGATATTATTTTACATTTCT  3366
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  TCTCAAAACAACAGAATACGATTTAGCAAATTACTTCTTAAGATATTATTTTACATTTCT  900

Qy  3367  ATATTCTCCTACCTGAGTTGATGTGTGTGAGCAATATGTCACTTCATAAAGCCAGGTATA  3426
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   901  ATATTCTCCTACCCTGAGTTGATGTGTGTGAGCAATATGTCACTTCATAAAGCCAGGTATA  960

Qy  3427  CATTATGGACAGGTAAGTAAAAAAACATATTATTATTCTCACGTTTTGTCCAAAAATTTT  3486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  CATTATGGACAGGTAAGTAAAAAAACATATTATTATTCTCACGTTTTGTCCAAAAATTTT  1020

Qy  3487  AAATTCAACTGTTGCCGTGTGTTGGTAATGTAAAACAAACTCAGTACAGTAGTATTCA  3546
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  AAATTCAACTGTTGCCGTGTGTTGGTAATGTAAAACAAACTCAGTACAGTAGTATTCA  1080

Qy  3547  GTACAGTATTTAAGCCCCTGTACTTAAACATATTCCTCCGTACCAATGAAGTTACATGAA  3606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  GTACAGTATTTAAGCCCCTGTACTTAAACATATTCCTCCGTACCAATGAAGTTACATGAA  1140

Qy  3607  AGCAAATTTGTGTGAGATATCGTAGATGGAAGTAAATTAGTCTTTATGTTCCCACAAAT  3666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db  1141  AGCAAATTTGTGTGAGATATCGTAGATGGAAGTAAATTAGTCTTTATGTTCCCACAAAT  1200

Qy  3667  TGAAATGCATTTCAAAAACTCTGTGTGTGATGTGTGTGATGTGTGTGACAGAGTGTGTGAGA  3726
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  1201  TGAAATGCATTTCAAAAACTCTGTGTGTGTATGTGTGTGTGTGTGTGACAGAGTGTGTGAGA  1260

Qy  3727  GAGAGACAGAGAGATACGGCTTTGGTTGCCTCCATAAGCTGGCTGCTATGATTAATAAGAC  3786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  GAGAGACAGAGAGATACGGCTTTGGTTGCCTCCATAAGCTGGCTGCTATGATTAATAAGAC  1320

Qy  3787  CAAGTTTTCTAAAGAAATGAGATCATAACAAAAGCCCTCTTTATGACTATCTTTATCA  3846
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db  1321  CAAGTTTTCTAAAGAAATGAGATCATAACAAAAGCCCTCTTTATGACTATCTTTTATCA  1380

Qy  3847  GGGGCAAAAAGGAAAGAGACAAAACAGCATGAAATGATGAGACCAAGTGATGAAAATTCA  3906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  GGGGCAAAAAGGAAAGAGACAAAACAGCATGAAATGATGAGACCAAGTGATGAAAATTCA  1440

Qy  3907  TTCACAATGATTGCTTCAAGAGTAATTCTCTTGGGTAATTCAGCACCTGTTACTATG  3966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  TTCACAATGATTGCTTCAAGAGTAATTCTCTTGGGTAATTCAGCACCTGTTACTATG  1500

Qy  3967  GCTCTCTGGAGTGATAGCTAATGTAAATGAAACAGAAATCCATTCAAAAGCATTCGGGAAAAATTCAAAAG  4026
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  GCTCTCTGGAGTGATAGCTAATGTAAATGAAACAGAAATCCATTCAAAAGCATTCGGGAAAAATTCAAAAG  1560

Qy  4027  ATATACTCAGCCAATAATGCAACAGAAATCCATTCAAAAGCATTCGGGAAAAATTCAAAAG  4086
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561  ATATACTCAGCCAATAATGCAACAGAAATCCATTCAACAGCATTGGATTATCCTGACAAGA  1620

Qy  4087  AATAAATATTCTTTTTTAAAGTTAATGACCTAGACCTTCATTCTCCCTGACT  4146
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  AATAAATATTCTTTTTTAAAGTTAATGACCTAGACCTTCATTCTCCCTGACT  1680

Qy  4147  AACAAGCAGCAAGCACTTAAAAATATCCAGCCAGGATGAAATAGAAAACCACCTGACTTG  4206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  AACAAGCAGCAAGCACTTAAAAATATCCAGCCAGGATGAAATAGAAAACCACCTGACTTG  1740

Qy  4207  TTAATATTTTGTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTGAATGATCTT  4266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  TTAATATTTTGTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTGAATGATCTT  1800

Qy  4267  GGCAAATGTCTCGAATTATTTGCCAACTTTCTTATCTTGGAAAAAAGTTCATGA  4326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  GGCAAATGTCTCGAATTATTTGCCAACTTTCTTATCTTGGAAAAAAGTTCATGA  1860

Qy  4327  ATGGGTGTCAAAATTGATTAGTTTAAAAACCTTCGCAGATACGTATGGCACCCTAA  4386
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  ATGGGTGTCAAAATTGATTAGTTTAAAAACCTTTGCAGATACGTATGGCACCCTAA  1920

Qy  4387  AACTGTATTAGAAAAAAAAGTAAGTACTCTGTAGTGTGAAAAATTCTTAAGGACACCCTC  4446
          ||||||||||||||||
Db  1921  AACTGTATTAGAAAAAA----------------------------------------  1938

Qy  4447  TTTTACAAACTCACAAAAACAGCCTTTGGAATACCCACCATGAAGTAGCTGTTGTTATTGC  4506
Db  1939  ------------------------------------------------------------  1938

Qy  4507  TTTCTATATACCTACATCTTGTCTATTATAAAAAGACTGGTTTTTGGCAGGTGTGGTGGC  4566
Db  1939  ------------------------------------------------------------  1938

Qy  4567  TCACACCTGTAATTCCAGCACTTTGGGAGGCCAAGGCGGGCGGGGGATCACCTGAGATCAGGA  4626
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Qy  5527 CCTGGGCAGAGCTGTTTTATTTCTCTATGCCGTGGAGAGAAATTGGTTAATTGGCCATGG 5586
Db  1939 ------------------------------------------------------------ 1938

Qy  5587 AAGGCAGTCATTAAGATGTTCCCATGCCGAGTGGATGAACTTTCCAGGGTTCCCAGCTTCTGCAT 5646
Db  1939 ------------------------------------------------------------ 1938

Qy  5647 CCTTCCCGTGTCCCTCAATTCATTGTTGGTGATGACAATGTCTCTCCATCAGCCTCATG 5706
Db  1939 ------------------------------------------------------------ 1938

Qy  5707 AAGTTCTCTCATTTATTAAAATTGCTTCAGGAAAAATTTTGAAAATGTGTCCAGTA 5766
Db  1939 ------------------------------------------------------------ 1938

Qy  5767 ATGCCTGATTGGCCCCTTATCCTCAAAGGCTTAAACTGAGGAAGGAAGCTAAACTGAGAA 5826
Db  1939 ------------------------------------------------------------ 1938

Qy  5827 ATCTTGCAAATCATTGAGCCAAAAACGTATTAATAGCAAGATCTATCATTTATTGACTAG 5886
Db  1939 ------------------------------------------------------------ 1938

Qy  5887 TATGTGGCAGGCAGTAGTGCCCTTTATTTAGGCAGGGAGAGTTGATGGGGGGGCGGGGTTC 5946
Db  1939 ------------------------------------------------------------ 1938

Qy  5947 ACACATCTTAAAGAGGTGCTATCTCCTCCTATATAAATCATGTAAGTCAAGAGAGTAAGG 6006
Db  1939 ------------------------------------------------------------ 1938

Qy  6007 AATTGTCTTGTTTGGTTATATTCAGGGGATTAGAGTATACAGTAGAAGATCCCAAGAAA 6066
Db  1939 ------------------------------------------------------------ 1938

Qy  6067 CCTTGGGATCATTTAGACTAAGAAATGCCAATACCCGCCGGCCGGGTCGGCTCACGCCTG 6126
Db  1939 ------------------------------------------------------------ 1938

Qy  6127 TAATCCCAGCACTTGAGAGGCCGAGGTGGGCGGATCACAAGGTCAGGAGATTGAGACCG 6186
Db  1939 ------------------------------------------------------------ 1938

Qy  6187 TCCTGGCTAACGTGGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTAGCCGGGCGGTG 6246
Db  1939 ------------------------------------------------------------ 1938

Qy  6247 GTGGCGGGCGCCTGTAGTCCCAGCTACTCGGGAGGCGGAGGAATGGTGTGAACT 6306
Db  1939 ------------------------------------------------------------ 1938

Qy  6307 CAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCCCCATGCACTCCAGCCTGGGCGACAG 6366
Db  1939 ------------------------------------------------------------ 1938

Qy  6367 AACGAGACTCCGTCTCAGAACAAAACAAAAGGAAATGCCAATACCAGCAGAAATAGAGCC 6426
Db  1939 ------------------------------------------------------------ 1938

Qy  6427 AAATCATGAACATAAGCTAAACAAATGTTGGCAGTGTAGCCTAGTGGTTAAGAGAGCAGA 6486
Db  1939 ------------------------------------------------------------ 1938
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Db  1939 -------------------------------------------------------------- 1938

Qy  7447 ATTATCAAGGGTCTCCAGTCATCTCCACATGTTCTTAATCATTATCTTCTTTACAGTT 7506
                                                              |||
Db  1939 ----------------------------------------------------------TTT 1941

Qy  7507 CATATCTCCAGGCCTTTCATTGGGTCAGGTTGGCATTTCGCTGCCCTTTATGTGTGTGAC 7566
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1942 CATATCTCCAGGCCTTTCATTGGGTCAGGTTGGCATTTCGCTGCCCTTTATGTGTGTGAC 2001

Qy  7567 AAGTGAAAATAAGGAAGAGAAAAAACTCAAGTGAAGAAAATCAGAATCTCGGCGCAGAGTT 7626
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2002 AAGTGAAAATAAGGAAGAGAAAAAACTCAAGTGAAGAAAATCAGAATCGCGGCGCAGAGTT 2061

Qy  7627 CCTGGGCGTTTCAGCTGCTTCCCACATCACCTGCCTCATCAAGCCCAGCATCCATCTCC 7686
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2062 CCTGGGCGTTTCAGCTGCTTCCCACATCACCTGCCTCATCAAGCCCCAGCATCCATCTCC 2121

Qy  7687 TTGCTCATCTTACACCCTGTGTGATGACAGGCCCACCATTCATTTATCAGAGCAAAGGC 7746
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2122 TTGCTCATCTTACACCCTGTGTGATGACAGGCCCACCATTCATTTATCAGAGCAAAGGC 2181

Qy  7747 TCTCCACTATTCTGGTTCACCCCCTACTTAGCCAGATATACAAGAATATCTGCACGGA 7806
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2182 TCTCCCACTATTCTGGTTCACCCCCTACTTAGCCAGATATACAAGAATATCTGCACGGA 2241

Qy  7807 TGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTATCGGCACCAAGGAC 7866
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2242 TGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTATCGGCACCAAGGAC 2301

Qy  7867 AGATCTCCCAGCAAGATGCACAGAAAAGACTAACTGCCCCCAAAATCTCCCTTCCAAAAC 7926
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2302 AGATCTCCCAGCAAGATGCACAGAAAAGACTAACTGCCCCCAAAATCTCCCTTCCAAAAC 2361

Qy  7927 ACAGTTCTCTTAATTCTCCCAAGCAAACCAGAATGTGACTGCTCACCTCCTCTAAGGACCTG 7986
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2362 ACAGTTCTCTTAATTCTCCCAAGCAAACCAGAATGTGACTGCTCACCTCCTCTAAGGACCTG 2421

Qy  7987 AAAACAACTGGCCATTTCAGCTATTTAAATCAACTTTAAAAAATCCAACCGCCAAAATAT 8046
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2422 AAAACAACTGGCCATTTCAGCTATTTAAATCAACTTTAAAAAATCCAACCGCCAAAATAT 2481

Qy  8047 TAAACCATTTGGTTGGAATGATAACATAACTAACCTGCTGACAGCTGCTTCTGCTAGGT 8106
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2482 TAAACCATTTGGTTGGAATGATAACATAACTAACCTGCTGACAGCTGCTTCTGCTAGGT 2541

Qy  8107 GCAAAAATGGAAAAAAAATACTTCTAATCAGGTCAAATCACTCACCTTTGGGATTCTA 8166
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2542 GCAAAAATGGAAAAAAAATACTTCTAATCAGGTCAAATCACTCACCTTTGGGATTCTA 2601

Qy  8167 AATTTACTCATATTCTCAAAGAAATATATTCAGTCATGTATGGTGGAAAATAGGATTATTCC 8226
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2602 AATTTACTCATATTCTCAAAGAAATATATTCAGTCATGTATGGTGGAAAATAGGATTATTCC 2661

Qy  8227 TTTAGCTCGATAAGGCAACCAGAAGTTCTTCCTTAATCATTTAATCAATCAATCAGAA 8286
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2662 TTTAGCTCGATAAGGCAACCAGAAGTTCTTCCTTCAAAATCTTAATCAATCAATCAGAA 2721

Qy  8287 ATTGATTTTTGGAAAACTGTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTCTTTA 8346
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2722 ATTGATTTTTGGAAAACTGTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTTCTTTA 2781

Qy  8347 CAATCCGAGATGAAGAGGAAATTCACAACCTGGACTTTCACCTCCATTGGTCAGAGTT 8406
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                        10535500-11_vs_10535500allna.txt

Qy  6487 CTCTTAACTAGAACACTGCACTCCATGTCCTCACTGTGACCCTCACTGTGGGGTTCTAA 6546
Db  1939 -------------------------------------------------------------- 1938

Qy  6547 TTAACCCCTGTTACTTACCAGTGGCAGTCTTAAGGCATTCCTTAAGTTCGTTGTGCCCCA 6606
Db  1939 -------------------------------------------------------------- 1938

Qy  6607 ATTTGTTCATCTGTAGAAGGGGTAGGATGACACAGTAGTGTTTACTTTATAGGCTTACTGTG 6666
Db  1939 -------------------------------------------------------------- 1938

Qy  6667 AGGATTAAATGAGTTACTACTGTATTTGTAAAGTGCTTAAAATGCTGCTCCAAAAGAGTT 6726
Db  1939 -------------------------------------------------------------- 1938

Qy  6727 TGTTAAACACTTAAGAACTGATTTACTTGCATCTAAACTGACAGCTCTCAATAACTGGAA 6786
Db  1939 -------------------------------------------------------------- 1938

Qy  6787 ATGATCAAGCATAGGCCCTGGAATATAAGCAGGTCTACATGAAGGCAAAAATGTTCGTTT 6846
Db  1939 -------------------------------------------------------------- 1938

Qy  6847 CTTTTGTTCAGCCCTGTGCCTAGATCAATATCTAGTGATCATGCTCAAGAAATATTGTTG 6906
Db  1939 -------------------------------------------------------------- 1938

Qy  6907 AATGAATCAATGAACCTACCGAGGTAGTTACATAAAAGAGTTCTGCGATGAGTACAAATCT 6966
Db  1939 -------------------------------------------------------------- 1938

Qy  6967 GGGCAAAGTGACCTCCAAGGAAATTTCCACTTTAGATTCTGTGATTTCCTTAAGGAACT 7026
Db  1939 -------------------------------------------------------------- 1938

Qy  7027 GATAAATTGGTGTGATACAATGTAAAAAATGTGCCTATATGATTTGAGAGAAAAACTTATT 7086
Db  1939 -------------------------------------------------------------- 1938

Qy  7087 TTCTCTCCCTCTTTTTCCTTCCTCCTCCCCCCTTCCTTCCTCCTCCTCCCT 7146
Db  1939 -------------------------------------------------------------- 1938

Qy  7147 TCCTTCCTCCCTCCCTTCCTTCCTTCCTTCTTCTTCTTCTTCTTCTTCTTC 7206
Db  1939 -------------------------------------------------------------- 1938

Qy  7207 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTCTCTTCTTTCCTTTCCTTCCT 7266
Db  1939 -------------------------------------------------------------- 1938

Qy  7267 TTCTTGTGCCTTCTTCTTCTTCTTCTCTCTGTCCTTTCTTTCTTTCTTT 7326
Db  1939 -------------------------------------------------------------- 1938

Qy  7327 CTTTCTGCCTTCTTCTTCTTCTCTCTTGTTTTTCTTTCTTCCTTTTTTCCTTTAAGCAGAC 7386
Db  1939 -------------------------------------------------------------- 1938

Qy  7387 CATGTCTGTTAGATGAATGCCTTTTCTAGTTAAAAGGTTAAACAGGAAAGTGAAGCACA 7446
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```
Qy   9307 GTTACCTAATCTCTCCAGGCCTCCATTTTCTTATCATTAAATGAAGATAATAAAAGTATT 9366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3742 GTTACCTAATCTCTCCAGGCCTCCATTTTCTTATCATTAAATGAAGATAATAAAAGTATT 3801

Qy   9367 TTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGC 9426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3802 TTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAGGGC 3861

Qy   9427 CCAGCCTATATTAATTTATCAATAAATGCCAG 9458
          ||||||||||||||||||||||||||||||||
Db   3862 CCAGCCTATATTAATTTATCAATAAATGCCAG 3893
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RESULT 6
US-10-535-500A-7
; Sequence 7, Application US/10535500A
; GENERAL INFORMATION:
; APPLICANT: Rigshospitalet
; APPLICANT: Henrik Leffers
; APPLICANT: Anne Mette Buhl Hertz
; APPLICANT: Jorgen Kjems
; TITLE OF INVENTION: Methods and kits for diagnosing and
; TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
; FILE REFERENCE: P34546US01
; CURRENT APPLICATION NUMBER: US/10/535,500A
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: DK/PA 200201792
; PRIOR FILING DATE: 2002-11-19
; SOFTWARE: FastSEQ for Windows version 4.0
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 7
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-535-500A-7

Query Match   20.7%; Score 1956; DB 1; Length 2817;
Best Local Similarity   99.5%; Pred. No. 6e-17;
Matches 1962; Conservative   0; Mismatches   10; Indels   0; Gaps   0;

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Qy   7487 ATTATCTCTTTACAGTTCATATCTCCAGGCCTTCATTGGGTCAGGTTGGCATTTCG 7546
          || ||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    846 ACTGTATTAGAAAAAATTTCATATCTCCAGGCCTTCATTGGGTCAGGTTGGCATTTCG 905

Qy   7547 CTGCCCTTTATGTGTGCAAGTGAAAATAAGGAAAGAAAAAACTCAAGTGAAGAAAA 7606
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    906 CTGCCCTTTATGTGTGCAAGTGAAAATAAGGAAAGAAAAAACTCAAGTGAAGAAAA 965

Qy   7607 TCAGAATCTGCGCAGCAGTTCCTGGGCGTTCAGCTGCTTCCCACATCACCTGCCTCATC 7666
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 TCAGAATCTGCGCAGCAGTTCCTGGGCGTTCAGCTGCTTCCCACATCACCTGCCTCATC 1025

Qy   7667 AAGCCCCAGCATCCATCTCCTTGCTCATCTTACACCCTGTGCATGACAGGCCCACCAT 7726
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 AAGCCCCAGCATCCATCTCCTTGCTCATCTTACACCCTGTGCATGACAGGCCCACCAT 1085

Qy   7727 TCATTTATCAGAGCAAAGGCTCTCCCACTATTCTCGTTCACCCCCTACTTAGCCAGATA 7786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 TCATTTATCAGAGCAAAGGCTCTCCCACTATTCTCGTTCACCCCCTACTTAGCCAGATA 1145

Qy   7787 TACAAGAATATCTGCACGGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCC 7846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1146 TACAAGAATATCTGCACGGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCC 1205
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Db   2782 CAATCCAGACTATAGAGAGGAAATTCACAACCTGGACTTTCACCTCCATTGGTCAGAGTT 2841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   8407 TACTGACCAATTCCCACCTCTGCCTTACACCTAACGGAAGTTATGCCTGTTTTCTTC 8466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2842 TACTGACCAATTCCCACCTCTGCCTTACACCTAACGGAAGTTATGCCTGTTTTCTTC 2901

Qy   8467 ACATACCCCAACAGTTACAAATGGTTGTATTATTAAGCATCTTTATTTGTGGCCTCT 8526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2902 ACATACCCCAACAGTTACAAATGGTTGTATTATTAAGCATCTTTATTTGTGGCCTCT 2961

Qy   8527 GATTACATGGTCCCCTAAATTTGACCTAATCACAAAGATTGGTAAAATTTCTTAACAT 8586
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2962 GATTACATGGTCCCCTAAATTTGACCTAATCACAAAGATTGGTAAAATTTCTTAACAT 3021

Qy   8587 ATTAATAATATTTTGTTTATGTGTCAATATCTTAGCATGTGATCAATTAAGACAGAGGTCT 8646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3022 ATTAATAATATTTTGTTTATGTGTCAATATCTTAGCATGTGATCAATTAAGACAGAGGTCT 3081

Qy   8647 TAACGTTCTCTTTTGAAAGAGAATATATAGGAATTCAGAGATATTAAGAGATTCTCCCAGG 8706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3082 TAACGTTCTCTTTTGAAAGAGAATATATAGGAATTCAGAGATATTAAGAGATTCTCCCAGG 3141

Qy   8707 ATCACAGTTAGGTAACAGAGCTGGATTTTAGTCCAGGTCTGTCTACAGCTCTAACGTATA 8766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3142 ATCACAGTTAGGTAACAGAGCTGGATTTTAGTCCAGGTCTGTCTACAGCTCTAACGTATA 3201

Qy   8767 TACACCCTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAAGTC 8826
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3202 TACACCCTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAAGTC 3261

Qy   8827 AGGGGTCAGCAACCTTTCTAAAAGGACCAAATAGTAATATTTCAGGCTTTGTGGACCC 8886
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3262 AGGGGTCAGCAACCTTTCTAAAAGGACCAAATAGTAATATTTCAGGCTTTGTGGACCC 3321

Qy   8887 TATGGTCTCTATCATAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAAGCAAAA 8946
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3322 TATGGTCTCTATCATAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAAGCAAAA 3381

Qy   8947 TATAAAACTAACGAAATGTGGCTGTTTTTTATGGATTTTTTTAACTCTTTATTTACAAAAG 9006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3382 TATAAAACTAACGAAATGTGGCTGTTTTTTATGGATTTTTTTAACTCTTTATTTACAAAAG 3441

Qy   9007 CAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTGAGAAAA 9066
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3442 CAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTGAGAAAA 3501

Qy   9067 TCTTATATTTATGGACAACATTTAGACTGTGACTTGCCAAGTAAGAACAAGAAAGCTCTGT 9126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3502 TCTTATATTTATGGACAACATTTAGACTGTGACTTGCCAAGTAAGAACAAGAAAGCTCTGT 3561

Qy   9127 CAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGT 9186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3562 CAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTGTTAATGATAAGT 3621

Qy   9187 GAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAGAATAATGACCATAGAC 9246
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3622 GAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAGAATAATGACCATAGAC 3681

Qy   9247 TCCTGAACAAGAATGTCTGCGACTTCTGGCACTCTTGTTGTATGGTCCAGGCCAA 9306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3682 TCCTGAACAAGAATGTCTGCGACTTCTGGCACTCTTGTTGTATGGTCCAGGCCAA 3741
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Qy  2106 GTCTACAGCTCTAACGTATATACACCCTTGTATAACATGTCACGAATTCAGCAGCATAAAGG 2165

Db  8807 GATCTTCAGTGATCTAAGTCAGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAAT 8866
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2166 GATCTTCAGTGATCTAAGTCAGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAAT 2225

Qy  8867 ATTTCAGGCTTGTGGACCCTATGCTCTCATCATAACTGTTCAAATCACCATGTAGTGT 8926
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2226 ATTTCAGGCTTGTGGACCCTATGCTCTCATCATAACTGTTCAAATCACCATGTAGTGT 2285

Qy  8927 AAAAGGAGCCATAAGCAAAATATAAACTACCGAATGTGTTGGCTGTTATGGGAT 8986
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2286 AAAAGGAGCCATAAGCAAAATATAAACTACCGAATGTGTTGGCTGTTATGGGAT 2345

Qy  8987 TAACTCTTTATTTACAAAAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTC 9046
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2346 TAACTCTTTATTTACAAAAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTC 2405

Qy  9047 TGACCCCTGACCTGAGAAAATCTTATATTTATGGACACACATTTAGACTGTGACTTGCCAA 9106
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2406 TGACCCCTGACCTGAGAAAATCTTATATTTATGGACACAACATTTAGACTGTGACTTGCCAA 2465

Qy  9107 GTAAGAACAAGAAGCTCTGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCT 9166
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2466 GTAAGAACAAGAAGCTCTGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCT 2525

Qy  9167 GTCTGGTGTTAATGATAAGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGACAC 9226
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2526 GTCTGGTGTTAATGATAAGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGACAC 2585

Qy  9227 AAAGAATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCACTCT 9286
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2586 AAAGAATAATGACCATAGACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCACTCT 2645

Qy  9287 TGTTGTATGGTCCAGGCCAAGTTACCTACCTATCTCTCCAGGCCTCCATTTCTTATCATTAA 9346
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2646 TGTTGTATGGTCCAGGCCAAGTTACCTACCTATCTCTCCAGGCCTCCATTTCTTATCATTAA 2705

Qy  9347 ATGAAGATAATAAAAGTATTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATG 9406
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2706 ATGAAGATAATAAAAGTATTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATG 2765

Qy  9407 TCAAGCACATAGAATAGGGCCCAGCCTATATTAATTTATCAATAAATGCCAG 9458
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2766 TCAAGCACATAGAATAGGGCCCAGCCTATATTAATTTATCAATAAATGCCAG 2817
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RESULT 7
US-10-535-500A-10
; Sequence 10, Application US/10535500A
; GENERAL INFORMATION:
; APPLICANT: Rigshospitalet
; APPLICANT: Henrik Leffers
; APPLICANT: Anne Mette Buhl Hertz
; APPLICANT: Jorgen Kjems
; TITLE OF INVENTION: Methods and kits for diagnosing and
; TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
; FILE REFERENCE: P34546US01
; CURRENT APPLICATION NUMBER: US/10/535,500A
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: DK/PA 200201792
; PRIOR FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 43

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Qy  7847 ATTACTATGGCACCAAGGACAGATCTCCCAGCAAGAATGACAGAAAAGACTAACTGCCCC 7906
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1206 ATTACTATGGCACCAAGGACAGATCTCCCAGCAAGAATGACAGAAAAGACTAACTGCCCC 1265

Qy  7907 CAAAATCTCCCTCCAAAACACAGTTCTCTAATTCTCCCAAGAAACCAGAATGTGACTG 7966
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1266 CAAAATCTCCCTCCAAAACACAGTTCTCTAATTCTCCCAAGAAACCAGAATGTGACTG 1325

Qy  7967 CTCACCTCTCTAAGGACCTGAAAACAACTGGCCATTTCAGCTATTTAAATCAACTTAAA 8026
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1326 CTCACCTCTCTAAGGACCTGAAAACAACTGGCCATTTCAGCTATTTAAATCAACTTAAA 1385

Qy  8027 AAATCCAACCGCAAAATATTAAACCATTTGGTTGGAATGATAACATAACTAACCTGCT 8086
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1386 AAATCCAACCGCCAAAATATTAAACCATTTGGTTGGAATGATAACATAACTAACCTGCT 1445

Qy  8087 GACAGCTGCTTCTGCTAGGTGCAAAAATGGAAAAAAAAATACTTCTAATCAGGTCAAATC 8146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1446 GACAGCTGCTTCTGCTAGGTGCAAAAATGGAAAAAAAAATACTTCTAATCAGGTCAAATC 1505

Qy  8147 ACTCTACCTTTGGGATTCTAAATTTACTCATATTCTCAAAGAAATATATTCAGTCATAGT 8206
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1506 ACTCTACCTTTGGGATTCTAAATTTACTCATATTCTCAAAGAAATATATTCAGTCATAGT 1565

Qy  8207 GGGGAAAATAGGATTATTCCTTAGCTCGATAAGCAACCAGAAGTTCTTCCTTCAAATCT 8266
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1566 GGGGAAAATAGGATTATTCCTTAGCTCGATAAGCAACCAGAAGTTCTTCCTTCAAATCT 1625

Qy  8267 TGACATTTAATCAGCAAATGATTTTTGGAAAACTGTTTCCTATGAAGCTATCTCTG 8326
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1626 TGACATTTAATCAGCAAATGATTTTTGGAAAACTGTTTCCTATGAAGCTATCTCTG 1685

Qy  8327 CCTGAAGGATTTTCTTTACAACTATAGAAGGAAATTCACAACCTGGACTTTC 8386
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1686 CCTGAAGGATTTTCTTTACAACTATAGAAGGAAATTCACAACCTGGACTTTC 1745

Qy  8387 ACCTCCATTGGTCAGAGTTTACTGACCAATTCCCACCTCTGCCTACACCTAACGGAAG 8446
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1746 ACCTCCATTGGTCAGAGTTTACTGACCAATTCCCACCTCTGCCTACACCTAACGGAAG 1805

Qy  8447 TTTATGCCTGTTTCTTCACATACCCCAACAGTTACAAATGGTTGTTATTACTATTAAGCA 8506
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1806 TTTATGCCTGTTTCTTCACATACCCCAACAGTTACAAATGGTTGTTATTACTATTAAGCA 1865

Qy  8507 TCTTTATTTGTGGCCTCTGATTACATGGTCCCCTAAATTTTGACCTAATCACAAAAGA 8566
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1866 TCTTTATTTGTGGCCTCTGATTACATGGTCCCCTAAATTTTGACCTAATCACAAAAGA 1925

Qy  8567 TTGGTAAAATTCTTAAACATATTAATAATATATTTGTTTATGTGTCAATATCTTAGCATGT 8626
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1926 TTGGTAAAATTCTTAAACATATTAATAATATATTTGTTTATGTGTCAATATCTTAGCATGT 1985

Qy  8627 ATCAATTAAGACAGAGGTCTTAACGTTCTCTTTTGAAAGAGAATATTAGGATTCAGAGA 8686
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1986 ATCAATTAAGACAGAGGTCTTAACGTTCTCTTTTGAAAGAGAATATTAGGATTCAGAGA 2045

Qy  8687 TATTAAGAGATTCTCCGGATCACAGTTAGGTAACACAGAGCTGGATTTTAGTCCGGTCT 8746
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2046 TATTAAGAGATTCTCCCAGGATCACAGTTAGGTAACACAGAGCTGGATTTTAGTCCGGTCT 2105

Qy  8747 GTCTACAGCTCTAACGTATATACACCCTTGTATAACATGTCACGAATTCAGCAGCATAAAGG 8806
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        10535500-11_vs_10535500allna.txt
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 1955
TYPE: DNA
ORGANISM: Homo sapiens
US-10-535-500A-10

Query Match     20.7%;  Score 1955;  DB 1;  Length 1955;
Best Local Similarity   100.0%;  Pred. No. 8.7e-17;
Matches 1955;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  7504 TTTCATATCTCCAGGCCTTCATTGGGTCAGGTTGGCATTCGCTGCCCTTTATGTGTGT 7563
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 TTTCATATCTCCAGGCCTTCATTGGGTCAGGTTGGCATTCGCTGCCCTTTATGTGTGT 60

Qy  7564 GACAAGTGAAAATAAGGAAGAAAAAAACTCAAGTGAAGAAATCAGAAATCTGCGCAGCA 7623
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GACAAGTGAAAATAAGGAAGAAAAAAACTCAAGTGAAGAAATCAGAAATCTGCGCAGCA 120

Qy  7624 GTTCCTGGGCGTTCAGCTGCTTCCCACATCACCTGCCTCATCAAGCCCCAGCATCCATC 7683
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GTTCCTGGGCGTTCAGCTGCTTCCCACATCACCTGCCTCATCAAGCCCCAGCATCCATC 180

Qy  7684 TCCTGCTCATCTTACACCCTGTGTGCATGACAGGCCCACCATTCATTTATCAGAGCAAA 7743
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCCTGCTCATCTTACACCCTGTGTGCATGACAGGCCCACCATTCATTTATCAGAGCAAA 240

Qy  7744 GGGCTCTCCCACTATTCTGGTTCACCCCCCTACTTAGCCAGATATACAAGAATATCGCAC 7803
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GGGCTCTCCCACTATTCTGGTTCACCCCCCTACTTAGCCAGATATACAAGAATATCTGCAC 300

Qy  7804 GGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTATCGCACCAAG 7863
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTATCGCACCAAG 360

Qy  7864 GACAGATCTCCCAGCAAGAATGACAGAAAAGACTAACTGCCCCCAAAATCTCCCTTCCAA 7923
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACAGATCTCCCAGCAAGAATGACAGAAAAGACTAACTGCCCCCAAAATCTCCCTTCCAA 420

Qy  7924 AACACAGTTCTTCTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTCTAAGGAC 7983
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AACACAGTTCTTCTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTCTAAGGAC 480

Qy  7984 CTGAAAACAACTGGCCATTTCAGCTATTTAAATCAACTTAAAAAATCCAACCGGCCAAAA 8043
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 CTGAAAACAACTGGCCATTTCAGCTATTTAAATCAACTTAAAAAATCCAACCGGCCAAAA 540

Qy  8044 TATTAAACCATTTTGGTGGAATGATAACATAACTAACCTGCTGACGCTGCTTCTGCTA 8103
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TATTAAACCATTTTGGTGGAATGATAACATAACTAACCTGCTGACGCTGCTTCTGCTA 600

Qy  8104 GGTGCAAAAATGGAAAAAAAAATACTTCTAATCAGGTCAAATCACTCACTTGGGATT 8163
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGTGCAAAAATGGAAAAAAAAATACTTCTAATCAGGTCAAATCACTCACTTGGGATT 660

Qy  8164 CTAAATTACTCATATTCTCAAAGAAATATATTCAGTCATAGTGGGGAAAATAGGATTAT 8223
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAATTACTCATATTCTCAAAGAAATATATTCAGTCATAGTGGGGAAAATAGGATTAT 720

Qy  8224 TCCTTTAGCTCGATAAGCAACCAGAAGTTCTTCCTTCAAAATCTTGACATTTAATCAATCA 8283
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TCCTTTAGCTCGATAAGCAACCAGAAGTTCTTCCTTCAAAATCTTGACATTTAATCAATCA 780

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Qy  8284 GAAATTGATTTTGGAAAACTGTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTTCTT 8343
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GAAATTGATTTTGGAAAACTGTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTTCTT 840

Qy  8344 TTACAATCCAGACTATAGAAGGAAATTCACAACCTGGACTTCACCTCCATTGGTCAGAG 8403
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTACAATCCAGACTATAGAAGGAAATTCACAACCTGGACTTCACCTCCATTGGTCAGAG 900

Qy  8404 TTTACTGACCAATTCCCACCTCTGCCTACACCTAACGGAAGTTATGCCTGTTTTCTC 8463
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TTTACTGACCAATTCCCACCTCTGCCTACACCTAACGGAAGTTATGCCTGTTTTCTC 960

Qy  8464 TTCACATACCCAACAGTACAAATGGTGTATTATTAAGCATCTTTATTTGTGGCC 8523
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TTCACATACCCCAACAGTACAAATGGTGTTGTTATTATTAAGCATCTTTATTTGTGGCC 1020

Qy  8524 TCTGATTACATGGTCCCCTAAATTGACCTAATCACAAAAGATTGGTAAAATTCTAA 8583
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TCTGATTACATGGTCCCCTAAATTTGACCTAATCACAAAAGATTGGTAAAATTCTAA 1080

Qy  8584 CATATTAATAATATATTTGTTTATGTGTCAATATCTTAGCACGTGTATCAATTAAGACAGAGG 8643
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 CATATTAATAATATATTTGTTTATGTGTCAATATCTTAGCATGTGTATCAATTAAGACAGAGG 1140

Qy  8644 TCTTAAGGTCTCTTTTGAAAGAGAATATTAGGATTCAGAGATATTAAGAGATTCTCCC 8703
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 TCTTAAGGTCTCTTTTGAAAGAGAATATTAGGATTCAGAGATATTAAGAGATTCTCCC 1200

Qy  8704 AGGATCACAGTTAGGTAACAGAGCTGGATTTTAGTCCAGGTCTGTCTACAGCTCTAACGT 8763
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 AGGATCACAGTTAGGTAACAGAGCTGGATTTTAGTCCAGGTCTGTCTACAGCTCTAACGT 1260

Qy  8764 ATATACACCCTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAA 8823
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 ATATACACCCTTGTATAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAA 1320

Qy  8824 GTCAGGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAATATTCAGGCTTGTGTGGA 8883
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 GTCAGGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAATATTCAGGCTTGTGTGGA 1380

Qy  8884 CCCTATGGTCTCTATCATAACTGTTCAAATCACCATGTCAGTGTAAAGGAGCCATAAGCA 8943
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CCCTATGGTCTCTATCATAACTGTTCAAATCACCATGTCAGTGTAAAGGAGCCATAAGCA 1440

Qy  8944 AAATAAAACTAACGAATGTGGCTGTTTTATGGGATTTTTTAACTCTTTATTTACAA 9003
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 AAATAAAACTAACGAATGTGGCTGTTTTATGGGATTTTTTTAACTCTTTATTTACAA 1500

Qy  9004 AAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTGAGA 9063
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 AAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTGAGA 1560

Qy  9064 AAATCTTATATTTATGGACAACATTAGACTGTGACTTGCCAAGTAAGAACAAGAAGCTC 9123
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 AAATCTTATATTTATGGACAACATTAGACTGTGACTTGCCAAGTAAGAACAAGAAGCTC 1620

Qy  9124 TGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCGTGGTTAATGATA 9183
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCGTGGTTAATGATA 1680

Qy  9184 AGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAGAATAATGACCATA 9243
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 AGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAGAATAATGACCATA 1740

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10535500-11_vs_10535500allna.txt

RESULT 8
US-10-535-500A-16
; Sequence 16, Application US/10535500A
; GENERAL INFORMATION:
; APPLICANT: Rigshospitalet
; APPLICANT: Henrik Leffers
; APPLICANT: Anne Mette Buhl Hertz
; APPLICANT: Jørgen Kjems
; TITLE OF INVENTION: Methods and kits for diagnosing and
; TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
; FILE REFERENCE: P34546US01
; CURRENT APPLICATION NUMBER: US/10/535,500A
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: DK/PA 200201792
; PRIOR FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1955
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-535-500A-16

Query Match   20.7%; Score 1955; DB 1; Length 1955;
Best Local Similarity 100.0%; Pred. No. 8.7e-17;
Matches 1955; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      7504 Qy  TTTCATATCTCCAGGCCTTCATTGGGTCAGGTGGCATTTCGCTGCCCTTTATGTGTGT 7563
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 Db  TTTCATATCTCCAGGCCTTCATTGGGTCAGGTGGCATTTCGCTGCCCTTTATGTGTGT 60

      7564 Qy  GACAAGTGAAAATAAGGAAAGAAAAAAACTCAAGTGAAGAAAATCAGAATCTGCGCAGCA 7623
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 Db  GACAAGTGAAAATAAGGAAAGAAAAAAACTCAAGTGAAGAAAATCAGAATCTGCGCAGCA 120

      7624 Qy  GTTCCTGGGCGTTCAGCTGCTTCCCACATCACCTGCCTCATCAAGCCCCAGCATCCATC 7683
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 Db  GTTCCTGGGCGTTCAGCTGCTTCCCACATCACCTGCCTCATCAAGCCCCAGCATCCATC 180

      7684 Qy  TCCTTGCTCATCTTACACCCTGTGTGCATGACGAGGCCCACCATTCATTTATCAGAGCAAA 7743
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 Db  TCCTTGCTCATCTTACACCCTGTGTGCATGACGAGGCCCACCATTCATTTATCAGAGCAAA 240

      7744 Qy  GGCTCTCCCACTATTCTGGTTCACCCCCTACTTAGCCAGATATACAAGAATATCTGCAC 7803
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

      9244 Qy  GACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCACTTCTTGTTGTATGGTCCAGGC 9303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1741 Db  GACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCACTTCTTGTTGTATGGTCCAGGC 1800

      9304 Qy  CAAGTTACCTAATCTCTCCAGGCCTCCATTTCTTATCATTAAATGAAGATAATAAAAGT 9363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1801 Db  CAAGTTACCTAATCTCTCCAGGCCTCCATTTTCTTATCATTAAATGAAGATAATAAAAGT 1860

      9364 Qy  ATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAG 9423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1861 Db  ATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAG 1920

      9424 Qy  GGCCCAGCCTATATTAATTTATCAATAAATGCCAG 9458
             |||||||||||||||||||||||||||||||||||
      1921 Db  GGCCCAGCCTATATTAATTTATCAATAAATGCCAG 1955
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       241 Qy  GGCTCTCCCATATTCTGGTTCACCCCCTACTTAGCCAGATATACAAGAATATCTGGAC 300

      7804 Db  GGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTATCGCACCAAG 7863
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       301 Db  GGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTATCGCACCAAG 360

      7864 Qy  GACAGATCTCCCAGCAAGAATGACAGAAAAGACTAACTGCCCCCAAAATCTCCTTCCAA 7923
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       361 Db  GACAGATCTCCCAGCAAGAATGACAGAAAAGACTAACTGCCCCCAAAATCTCCTTCCAA 420

      7924 Qy  AACACAGTTCTCTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTCTAAGGAC 7983
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       421 Db  AACACAGTTCTCTTAATTCTCCCAAGAAACCAGAATGTGACTGCTCACCTCTCTAAGGAC 480

      7984 Qy  CTGAAAACAACTGGCCATTCAGCTATTTAAATCAACTTAAAAAATCCAACCGCCAAAA 8043
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       481 Db  CTGAAAACAACTGGCCATTCAGCTATTTAAATCAACTTAAAAAATCCAACCGCCAAAA 540

      8044 Qy  TATTAAACCATTTGGTGGAATGATAACATAACTAACCTGCTGACAGCTGCTTCTGCTA 8103
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       541 Db  TATTAAACCATTTGGTGGAATGATAACATAACTAACCTGCTGACAGCTGCTTCTGCTA 600

      8104 Qy  GGTGCAAAATGGAAAAAAAATACTTCTAATCAGGTCAAATCACTCACCTTTGGGATT 8163
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       601 Db  GGTGCAAAATGGAAAAAAAATACTTCTAATCAGGTCAAATCACTCACCTTTGGGATT 660

      8164 Qy  CTAAATTTACTACATATTCTCAAAGAAAATATATTCAGTCATAGTGGGGAAAATAGGATTAT 8223
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       661 Db  CTAAATTTACTACATATTCTCAAAGAAAATATATTCAGTCATAGTGGGGAAAATAGGATTAT 720

      8224 Qy  TCCTTTAGTCGATAAGCAACCAGAAGTTCTTCCTCAAATCTTGACATTTAATCATCA 8283
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       721 Db  TCCTTTAGTCGATAAGCAACCAGAAGTTCTTCCTCAAATCTTGACATTTAATCAATCA 780

      8284 Qy  GAAATTGATTTTCCTATGAAGCTATCTCCGCCTGAAGGATTTTCTT 8343
             ||||||||||||||||||||||||||||||||||||||||||||||
       781 Db  GAAATTGATTTTCCTATGAAGCTATCTCCGCCTGAAGGATTTTCTT 840

      8344 Qy  TTACAATCCAGACTATAGAAGGAAATTCACAACCTGGACTTCACCTCCATTGGTCAGAG 8403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       841 Db  TTACAATCCAGACTATAGAAGGAAATTCACAACCTGGACTTCACCTCCATTGGTCAGAG 900

      8404 Qy  TTTACTGACCAATTCCCACCTCGCCTTACACCTAACGGAAGTTATGCCGTTTCTC 8463
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
       901 Db  TTTACTGACCAATTCCCACCTCGCCTTACACCTAACGGAAGTTATGCCGTTTCTC 960

      8464 Qy  TTCACATACCCCAACAGTTACAAATGGTTGTTATTATTAAGGCATCTTTTATTTGTGGCC 8523
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       961 Db  TTCACATACCCCAACAGTTACAAATGGTTGTTATTATTAAGGCATCTTTTATTTGTGGCC 1020

      8524 Qy  TCTGATTACATGGTCCCCTAAATTTTGACCTAATCACAAAAGATTGGTAAAATTCTTAA 8583
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1021 Db  TCTGATTACATGGTCCCCTAAATTTTGACCTAATCACAAAAGATTGGTAAAATTCTTAA 1080

      8584 Qy  CATATTAATAATATTTTGTTATGTCAATATCTTAGCATGTATCAATTAAGACAGAGG 8643
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1081 Db  CATATTAATAATATTTTGTTATGTCAATATCTTAGCATGTATCAATTAAGACAGAGG 1140

      8644 Qy  TCTTAAGCTTCTTTTGAAAGAGAATATTAGGATTCAGAGATATTAAGAGATTCTCCC 8703
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      1141 Db  TCTTAAGCTTCTTTTGAAAGAGAATATTAGGATTCAGAGATATTAAGAGATTCTCCC 1200

      8704 Qy  AGGATCACAGTTAGGTAACAGAGCTGGATTTAGTCCAGGTCTGTCTACAGCTCTAACGT 8763
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                    10535500-11_vs_10535500al1na.txt

SEQ ID NO 6
  LENGTH: 2260
  TYPE: DNA
  ORGANISM: Homo sapiens
US-10-535-500A-6

Query Match      20.7%;  Score 1955;  DB 1;  Length 2260;
Best Local Similarity  100.0%;  Pred. No. 7.5e-17;
Matches 1955;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  7504 TTCATATCTCCAGGCCTTTCATTGGGTCAGGTTGGCATTTGGCTGCCCTTTATGTGTGT 7563
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 TTCATATCTCCAGGCCTTTCATTGGGTCAGGTTGGCATTTGGCTGCCCTTTATGTGTGT  365

Qy  7564 GACAAGTGAAAATAAGGAAAGAAAAAAACTCAAGTGAAGAAAATCAGAATCTGCGCAGCA 7623
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 GACAAGTGAAAATAAGGAAAGAAAAAAACTCAAGTGAAGAAAATCAGAATCTGCGCAGCA  425

Qy  7624 GTTCCTGGGCGTTTCAGCTGCTCCCACATCACCTGCTCATCAAGCCCCAGCCCATC 7683
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   426 GTTCCTGGGCGTTTCAGCTGCTCCCACATCACCTGCTCATCAAGCCCCAGCATCCATC  485

Qy  7684 TCCTTGCTCATCTTACACCCTGTGTGCATGACAGGCCCACCATTCATTTATCAGAGCAAA 7743
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 TCCTTGCTCATCTTACACCCTGTGTGCATGACAGGCCCACCATTCATTTATCAGAGCAAA  545

Qy  7744 GGCTCTCCACTATTCTGGTTCACCCCCCTACTTAGCCAGATATACAAGAATATCTGCAC 7803
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 GGCTCTCCACTATTCTGGTTCACCCCCCTACTTAGCCAGATATACAAGAATATCTGCAC  605

Qy  7804 GGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTACTGGCACCAAG 7863
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   606 GGATGACCTGCCTCACCTGGGAGCTCAGAGGAGCTCAGATTCCATTACTACTGGCACCAAG  665

Qy  7864 GACAGATCTCCCAGCAAGAATGACAGAGAAAAGACTAACTGCCCCAAATCTCCCTTCCAA 7923
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 GACAGATCTCCCAGCAAGAATGACAGAGAAAAGACTAACTGCCCCAAATCTCCCTTCCAA  725

Qy  7924 AACACAGTTCTCTTAATTCTCCAAGAAACCAGAATGTGACTGCTCACCTCTCTAAGGAC 7983
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   726 AACACAGTTCTCTTAATTCTCCAAGAAACCAGAATGTGACTGCTCACCTCTCTAAGGAC  785

Qy  7984 CTGAAAACAACTGGCCATTTCAGCTATTAAATCAACTTAAAAAATCAACCGCCAAAA 8043
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   786 CTGAAAACAACTGGCCATTTCAGCTATTAAATCAACTTAAAAAATCAACCGCCAAAA  845

Qy  8044 TATTAAACCATTTTGGTTGGAATGATAACATAACTAACCTGCTGACAGCTGCTTCTGCTA 8103
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   846 TATTAAACCATTTTGGTTGGAATGATAACATAACTAACCTGCTGACAGCTGCTTCTGCTA  905

Qy  8104 GGTGCAAAATGGAAAAAAAATACTTCTAATCAGGTCAAATCACTCTACCTTTGGGATT 8163
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   906 GGTGCAAAATGGAAAAAAAATACTTCTAATCAGGTCAAATCACTCTACCTTTGGGATT  965

Qy  8164 CTAAATTTACTCATATTCTCAAAGAAATATATTCAGTCATAGTGGGGAAAATAGGATTAT 8223
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   966 CTAAATTTACTCATATTCTCAAAGAAATATATTCAGTCATAGTGGGGAAAATAGGATTAT 1025

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                    10535500-11_vs_10535500al1na.txt

Db 1201 AGGATCACAGTTAGGTAACAGAGCTGGATTTTAGTCCAGGTCTGTCTACAGCTCTAACGT 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 8764 ATATACACCCTTTGTATAAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAA 8823
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 ATATACACCCTTTGTATAAACATGTCACGAATTCAGCATAAAGGGATCTTCAGTGATCTAA 1320

Qy 8824 GTCAGGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAATATTTCAGGCTTTGTGGA 8883
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 GTCAGGGGTCAGCAACCTTTCTAAAAAGGACCAAATAGTAATATTTCAGGCTTTGTGGA 1380

Qy 8884 CCCTATGGTCTCATCATAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAAGCA 8943
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 CCCTATGGTCTCATCATAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAAGCA 1440

Qy 8944 AAATATAAACTAACGAATGTGGCTGTTTATGGGATTTTTTAACTCTTTATTTACAA 9003
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 AAATATAAACTAACGAATGTGGCTGTTTATGGGATTTTTTAACTCTTTATTTACAA 1500

Qy 9004 AAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTGAGA 9063
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501 AAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTGAGA 1560

Qy 9064 AAATCTTATATTTATGGACAACATTTAGACTGTGACTTGCCAAGTAAGAACAAGAAGCTC 9123
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561 AAATCTTATATTTATGGACAACATTTAGACTGTGACTTGCCAAGTAAGAACAAGAAGCTC 1620

Qy 9124 TGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTTAATGATA 9183
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621 TGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAAGAGCTGTCTGGTTAATGATA 1680

Qy 9184 AGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAGAATAATGACCATA 9243
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681 AGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGCACAAAGAATAATGACCATA 1740

Qy 9244 GACTCCTGAACAAGAATGTCTGGACTTCTGGACTTCTGTTGTATGGTCCAGGC 9303
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1741 GACTCCTGAACAAGAATGTCTGGACTTCTGGACTTCTGTTGTATGGTCCAGGC 1800

Qy 9304 CAAGTTACCTAACTCTCCAGGCCTCCATTTCTTATCATTAAATGAAGATAATAAAAGT 9363
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801 CAAGTTACCTAACTCTCCAGGCCTCCATTTCTTATCATTAAATGAAGATAATAAAAGT 1860

Qy 9364 ATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAG 9423
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1861 ATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAG 1920

Qy 9424 GGCCCAGCCTATATTAATTTATCAATAAATGCCAG 9458
        |||||||||||||||||||||||||||||||||||
Db 1921 GGCCCAGCCTATATTAATTTATCAATAAATGCCAG 1955
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RESULT 9
US-10-535-500A-6
; Sequence 6, Application US/10535500A
; GENERAL INFORMATION:
; APPLICANT: Rigshospitalet
; APPLICANT: Henrik Leffers
; APPLICANT: Anne Mette Buhl Hertz
; APPLICANT: Jorgen Kjems
; TITLE OF INVENTION: Methods and kits for diagnosing and
; TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)

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Qy 8224 TCCTTTAGCTCGATAAGCAACCAGAAGTTCTTCCTTCAAATCTTGACATTTAATCAATCA 8283
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1026 TCCTTTAGCTCGATAAGCAACCAGAAGTTCTTCCTTCAAATCTTGACATTTAATCAATCA 1085

Qy 8284 GAAATTGATTTTGGAAAAACTGTTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTCTT 8343
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1086 GAAATTGATTTTGGAAAAACTGTTTCCTATGAAGCTATCTCTGCCTGAAGGATTTTCTT 1145

Qy 8344 TACAATCCAGACTATAGAAGGAAATTCACAACCTGGACTTTCACCTCCATTGGTCAGAG 8403
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1146 TACAATCCAGACTATAGAAGGAAATTCACAACCTGGACTTTCACCTCCATTGGTCAGAG 1205

Qy 8404 TTTACTGACCAATTCCCACCTCTGCCTACACCTAACGGAAGTTTATGCCTGTTTTCTC 8463
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1206 TTTACTGACCAATTCCCACCTCTGCCTACACCTAACGGAAGTTTATGCCTGTTTTCTC 1265

Qy 8464 TTCACATACCCCAACAGTTACAAATGGTTGTTATTATTAAGCATCTTTATTTGTGGCC 8523
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1266 TTCACATACCCCAACAGTTACAAATGGTTGTTATTATTAAGCATCTTTATTTGTGGCC 1325

Qy 8524 TCTGATTACATGGTCTCCCTAAATTTTGACCTAATCACAAAAGATTGGTAAAATTTCTTAA 8583
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1326 TCTGATTACATGGTCTCCCTAAATTTTGACCTAATCACAAAAGATTGGTAAAATTTCTTAA 1385

Qy 8584 CATATTAATAATATTTGTTATGTGTCAATATCTTAGCATGTATCAATTAAGACAGAGAG 8643
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1386 CATATTAATAATATTTGTTATGTGTCAATATCTTAGCATGTATCAATTAAGACAGAGAG 1445

Qy 8644 TCTTAAGGTCTCTTTTGAAAGAGAATTAGGATTCAGAGATATTAAGAGATTCTCCC 8703
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1446 TCTTAAGGTCTCTTTTGAAAGAGAATTAGGATTCAGAGATATTAAGAGATTCTCCC 1505

Qy 8704 AGGATCACAGTTAGGTAACAGAGCTGGATTTTAGTCCAGGTCGTCTACAGCTCTAACGT 8763
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1506 AGGCACAGTTAGGTAACAGAGCTGGATTTTAGTCCAGGTCGTCTACAGCTCTAACGT 1565

Qy 8764 ATATACACCCCTTGTATAAACATGTCACGAATTCAGCATAAAAGGGATCTTCAGTGATCTAA 8823
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1566 ATATACACCCCTTGTATAAACATGTCACGAATTCAGCATAAAAGGGATCTTCAGTGATCTAA 1625

Qy 8824 GTCAGGGGTCAGCAACCTTTTCTAAAAAGGACCAAATAGTAATATTTCAGGCGTTTGTGGA 8883
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1626 GTCAGGGGTCAGCAACCTTTTCTAAAAAGGACCAAATAGTAATATTTCAGGCGTTTGTGGA 1685

Qy 8884 CCCTATGGTCTCTATCATAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAAGCA 8943
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1686 CCCTATGGTCTCATCATAACTGTTCAAATCACCATGTAGTGTAAAAGGAGCCATAAGCA 1745

Qy 8944 AAATATAAACTAACGAATGTGGCTGTTTATGGGATTTTTTAACTCTTTATTTTACAA 9003
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1746 AAATATAAACTAACGAATGTGGCTGTTTATGGGATTTTTTAACTCTTTATTTTACAA 1805

Qy 9004 AAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTGAGA 9063
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1806 AAGCAGGTGGCAGATCAGAACTCACTTATGGGCCATAGTTCTCTGACCCCTGACCTGAGA 1865

Qy 9064 AAATCTTATATTTATGGCACAACATTAGACTGTGACTTGCCAAGTAAGAACAAGAAGCTC 9123
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1866 AAATCTTATATTTATGGCACAACATTAGACTGTGACTTGCCAAGTAAGAACAAGAAGCTC 1925

Qy 9124 TGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAGAGCGTCTCGTTGGTGTTAATGATA 9183
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

10535500-11_vs_10535500allna.txt

```
Db 1926 TGTCAACTGAAGGTCAAGGCTGGAGTTCTGAAAGCAAGAGCGTCTCGTTGGTGTTAATGATA 1985
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 9184 AGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGGACAAAGAATAATGACCATA 9243
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1986 AGTGAAATAGTTAAAGTTAGAAGATCCCAGTTATAAGAAGGACAAAGAATAATGACCATA 2045

Qy 9244 GACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCACTCTTGTTGTATGGTCCAGGC 9303
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2046 GACTCCTGAACAAGAATGTCTGGACTTCTGGCTTAGGCACTCTTGTTGTATGGTCCAGGC 2105

Qy 9304 CAAGTTACCTAATCTCTCCAGGCCTCCATTTCTTATCATTAAATGAAGATAATAAAAGT 9363
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2106 CAAGTTACCTAATCTCTCCAGGCCTCCATTTCTTATCATTAAATGAAGATAATAAAAGT 2165

Qy 9364 ATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAG 9423
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2166 ATTTTCCTCAGAGAGCTGTAAGAATAAACTGAGCTAACCCATGTCAAGCACATAGAATAG 2225

Qy 9424 GGCCAGCCTATATTAATTTATCAATAAATGCCAG 9458
        ||||||||||||||||||||||||||||||||||
Db 2226 GGCCCAGCCTATATTAATTTATCAATAAATGCCAG 2260
```

RESULT 10
US-10-535-500A-15
; Sequence 15, Application US/10535500A
; GENERAL INFORMATION:
; APPLICANT: Rigshospitalet
; APPLICANT: Henrik Leffers
; APPLICANT: Anne Mette Buhl Hertz
; APPLICANT: Jorgen Kjems
; TITLE OF INVENTION: Methods and kits for diagnosing and
; TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
; FILE REFERENCE: P34546US01
; CURRENT APPLICATION NUMBER: US/10/535,500A
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: DK/PA 200201792
; PRIOR FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-535-500A-15

Query Match   5.9%; Score 557; DB 1; Length 557;
Best Local Similarity   100.0%; Pred. No. 0.0019; Indels 0; Gaps 0;
Matches 557; Conservative 0; Mismatches 0;

```
Qy 3848 GGGCAAAAGGAAAGAGACAAAACAGCATGAAATGATGAGACCAAGTGATGAAAATTCAT 3907
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GGGCAAAAAGGAAAGAGAGACAAAACAGCATGAAATGATGAGACCAAGTGATGAAAATTCAT 60

Qy 3908 TCACAATGATTGCTTCAAGAGTAATTTCTCTGGGTAATTCAGCAGCCTGTTTACTATGG 3967
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCACAATGATTGCTTCAAGAGTAATTTCTCTGGGTAATTCAGCAGCCTGTTTACTATGG 120

Qy 3968 CTCTCGGAGTGATAGCTAATGTAAATGAAGCCTCAAAAGTGGATTATCCTGACAAGAA 4027
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CTCTCGGAGTGATAGCTAATGTAAATGAAGCCTCAAAAGTGGATTATCCTGACAAGAA 180

Qy 4028 TATACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAATTCAAAAGA 4087
```

```
Db   181 TATACTCAGCCAATAATGCAACAGAAATCCATTCAAAGCATTCGGGAAAATTCAAAAGA 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 4088 ATAAATATTCTTT        TAAAGTAATGACCTACGATCCATTCTTCCCTGACTA 4147
         ||||||||||||||        ||||||||||||||||||||||||||||||||||||
Db   241 ATAAATATTCTTT        TAAAGTAATGACCTACGATCCATTCTTCCCTGACTA 300
Qy 4148 ACAAGCAGCAAGCACTTAAAAAATATCCAGCCAGGATGAAATAGAAACCCACCTGACTTGT 4207
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ACAAGCAGCAAGCACTTAAAAAATATCCAGCCAGGATGAAATAGAAACCCACCTGACTTGT 360
Qy 4208 TAATATTTTGTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTGAATGATCTTG 4267
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TAATATTTTGTTGGTCCCAGGGACTCAGATTCTAAGCCAAATTCTTGAATGATCTTG 420
Qy 4268 GCAAATGTCTCGAATTATTTTGCCAACTTTTCTTATCTTGGAAAAAAAAGTTCATGAA 4327
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GCAAATGTCTCGAATTATTTTGCCAACTTTTCTTATCTTGGAAAAAAAAGTTCATGAA 480
Qy 4328 TGGGTGTCAAAATGATTAGTTTAAAAACCTTTCTGCAGATACGTATGGCACCCTAA 4387
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGGGTGTCAAAATGATTAGTTTAAAAACCTTTCTGCAGATACGTATGGCACCCTAA 540
Qy 4388 ACTGTATTAGAAAAAAA 4404
         |||||||||||||||||
Db   541 ACTGTATTAGAAAAAAA 557
```

RESULT 11
US-10-535-500A-18
; Sequence 18, Application US/10535500A
; GENERAL INFORMATION:
;   APPLICANT: Rigshospitalet
;   APPLICANT: Henrik Leffers
;   APPLICANT: Anne Mette Buhl Hertz
;   APPLICANT: Jorgen Kjems
;   TITLE OF INVENTION: Methods and kits for diagnosing and
;   TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
;   FILE REFERENCE: P34546US01
;   CURRENT APPLICATION NUMBER: US/10/535,500A
;   CURRENT FILING DATE: 2005-05-18
;   PRIOR APPLICATION NUMBER: DK/PA 200201792
;   PRIOR FILING DATE: 2002-11-19
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 366
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-535-500A-18

Query Match   3.9%; Score 366; DB 1; Length 366;
Best Local Similarity   100.0%; Pred. No. 0.16;
Matches 366; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy 3151 ATGTTCAACAAATGCTCCTTTCATTCCTCTATTTACAGACCTGCCGCAGCAATTCTGCT 3210
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGTTCAACAAATGCTCCTTTCATTCCTCTATTTACAGACCTGCCGCAGCAATTCTGCT 60
Qy 3211 AGCAGCCTTTGTGCTATTATCTGTTTCTAAACTTAGTAATTGAGTGTGATCGGGAGACT 3270
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AGCAGCCTTTGTGCTATTATCTGTTTCTAAACTTAGTAATTGAGTGTGATCGGGAGACT 120
```

```
Qy 3271 AACTCTGAAATAAATAAGCTGATTATTTATTTCTCAAAACAACAGAATACGATTT 3330
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AACTCTGAAATAAATAAGCTGATTATTTATTTCTCAAAACAACAGAATACGATTT 180
Qy 3331 AGCAAATTACTTCTTAAGATATTATTTACATTCTATATTCTCCTACCCTGAGTGATG 3390
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGCAAATTACTTCTTAAGATATTATTTACATTCTATATTCTCCTACCCTGAGTGATG 240
Qy 3391 TGTGAGCAATATGTCACTTCATAAAGCCAGGTATACATTATGGACAGGTAAGTAAAAA 3450
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGTGAGCAATATGTCACTTCATAAAGCCAGGTATACATTATGGACAGGTAAGTAAAAA 300
Qy 3451 CATATTATTTATTCTACGTTTTGTCCAAAAATTTAAATTTCAACTGTTGCGGCGTGT 3510
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CATATTATTTATTCTACGTTTTGTCCAAAAATTTAAATTTCAACTGTTGCGGCGTGT 360
Qy 3511 TGGTAA 3516
         ||||||
Db   361 TGGTAA 366
```

RESULT 12
US-10-535-500A-14
; Sequence 14, Application US/10535500A
; GENERAL INFORMATION:
;   APPLICANT: Rigshospitalet
;   APPLICANT: Henrik Leffers
;   APPLICANT: Anne Mette Buhl Hertz
;   APPLICANT: Jorgen Kjems
;   TITLE OF INVENTION: Methods and kits for diagnosing and
;   TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
;   FILE REFERENCE: P34546US01
;   CURRENT APPLICATION NUMBER: US/10/535,500A
;   CURRENT FILING DATE: 2005-05-18
;   PRIOR APPLICATION NUMBER: DK/PA 200201792
;   PRIOR FILING DATE: 2002-11-19
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 307
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-535-500A-14

Query Match   3.2%; Score 307; DB 1; Length 307;
Best Local Similarity   100.0%; Pred. No. 0.64;
Matches 307; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 ATTTGAATTGGTGAACTTAGTAAAGCAGCAGCGGCTCTCACCAATAAGGGCAGGCATCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATTTGAATTGGTGAACTTAGTAAAGCAGCAGCGGCTCTCACCAATAAGGGCAGGCATCC 60
Qy   61 AATCTGTGAAAGCTTGAATAAAACAAAAGAGGAAAATTGCTTCTTTTCTTCT 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATCTGTGAAAGCTTGAATAAAACAAAAGAGGAAAATTGCTTCTTTTCTTCT 120
Qy  121 TGATCTAGTATATCATCTTCCTGCCCTTGGATGTGAGTGGGCCTTCAGACTTAAACCA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TGATCTAGTATATCATCTTCCTGCCCTTGGATGTGAGTGGGCCTTCAGACTTAAACCA 180
Qy  181 GGAGTTACACCCTTGGCTTCAGTTCTTCAGTTCTTGGACTTGGACTGAATTACACTG 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GGAGTTACACCCTTGGCTTCAGTTCTTCAGTTCTTGGACTTGGACTGAATTACACTG 240
```

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Qy 241 CCAGGTTTCCTGGTTCCTGGTTCTCCAGCTTGCAGATGGCAGATCATGGGACTTCTTGGCCTCCATA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CCAGGTTTCCTGGTTCCTGGTTCTCCAGCTTGCAGATGGCAGATCATGGGACTTCTTGGCCTCCATA 300

Qy 301 ATTGTGT 307
         |||||||
Db 301 ATTGTGT 307

RESULT 13
US-10-535-500A-8
; Sequence 8, Application US/10535500A
; GENERAL INFORMATION:
;   APPLICANT: Rigshospitalet
;   APPLICANT: Henrik Leffers
;   APPLICANT: Anne Mette Buhl Hertz
;   APPLICANT: Jorgen Kjems
;   TITLE OF INVENTION: Methods and kits for diagnosing and
;   TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
;   FILE REFERENCE: P34546US01
;   CURRENT APPLICATION NUMBER: US/10/535,500A
;   CURRENT FILING DATE: 2005-05-18
;   PRIOR APPLICATION NUMBER: DK/PA 200201792
;   PRIOR FILING DATE: 2002-11-19
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 1970
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-535-500A-8

Query Match   3.2%; Score 307; DB 1; Length 1970;
Best Local Similarity   100.0%; Pred. No. 0.11;
Matches 307; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATTTGAATTGGTGAACTTAGTAAAGCAGACGGCTCTCACCAATAAGGGCAGGCATCATCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATTTGAATTGGTGAACTTAGTAAAGCAGACGGCTCTCACCAATAAGGGCAGGCATCATCC 60

Qy   61 AATCTGTCGAAAGCTTGAATAAACAAAAAGAGGAAGGGAAATTTGCTTCTTTCTTCT 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATCTGTCGAAAGCTTGAATAAACAAAAAGAGGAAGGGAAATTTGCTTCTTTCTTCT 120

Qy 121 TGATCTAGTATATCATCTTCTCCGCCCTTGGATGTGAGTGGGCCTTAAACCA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TGATCTAGTATATCATCTTCTCCGCCCTTGGATGTGAGTGGGCCTTAAACCA 180

Qy 181 GGAGTTACACCCTTGGCTTCTCAGTTCTCAGTTCTTGGACTGAATTACACTG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GGAGTTACACCCTTGGCTTCTCAGTTCTCAGTTCTTGGACTGAATTACACTG 240

Qy 241 CCAGGTTTCCTGGTTCCTGGTTCTCCAGCTTGCAGATGGCAGATCATGGGACTTCTTGGCCTCCATA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CCAGGTTTCCTGGTTCCTGGTTCTCCAGCTTGCAGATGGCAGATCATGGGACTTCTTGGCCTCCATA 300

Qy 301 ATTGTGT 307
         |||||||
Db 301 ATTGTGT 307

RESULT 14

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US-10-535-500A-13
; Sequence 13, Application US/10535500A
; GENERAL INFORMATION:
;   APPLICANT: Rigshospitalet
;   APPLICANT: Henrik Leffers
;   APPLICANT: Anne Mette Buhl Hertz
;   APPLICANT: Jorgen Kjems
;   TITLE OF INVENTION: Methods and kits for diagnosing and
;   TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
;   FILE REFERENCE: P34546US01
;   CURRENT APPLICATION NUMBER: US/10/535,500A
;   CURRENT FILING DATE: 2005-05-18
;   PRIOR APPLICATION NUMBER: DK/PA 200201792
;   PRIOR FILING DATE: 2002-11-19
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 305
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-535-500A-13

Query Match   3.2%; Score 305; DB 1; Length 305;
Best Local Similarity   100.0%; Pred. No. 0.68;
Matches 305; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATTTGAATTGGTGAACTTAGTAAAGCAGACGGCTCTCACCAATAAGGGCAGGCATCATCC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATTTGAATTGGTGAACTTAGTAAAGCAGACGGCTCTCACCAATAAGGGCAGGCATCATCC 60

Qy   61 AATCTGTCGAAAGCTTGAATAAACAAAAAGAGGAAGGGAAATTTGCTTCTTTCTTCT 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 AATCTGTCGAAAGCTTGAATAAACAAAAAGAGGAAGGGAAATTTGCTTCTTTCTTCT 120

Qy 121 TGATCTAGTATATCATCTTCTCCGCCCTTGGATGTGAGTGGGCCTTAAACCA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TGATCTAGTATATCATCTTCTCCGCCCTTGGATGTGAGTGGGCCTTAAACCA 180

Qy 181 GGAGTTACACCCTTGGCTTCTCAGTTCTCAGTTCTTGGACTGAATTACACTG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GGAGTTACACCCTTGGCTTCTCAGTTCTCAGTTCTTGGACTGAATTACACTG 240

Qy 241 CCAGGTTTCCTGGTTCCTGGTTCTCCAGCTTGCAGATGGCAGATCATGGGACTTCTTGGCCTCCATA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 CCAGGTTTCCTGGTTCCTGGTTCTCCAGCTTGCAGATGGCAGATCATGGGACTTCTTGGCCTCCATA 300

Qy 301 ATTGT 305
         |||||
Db 301 ATTGT 305

RESULT 15
US-10-535-500A-5/c
; Sequence 5, Application US/10535500A
; GENERAL INFORMATION:
;   APPLICANT: Rigshospitalet
;   APPLICANT: Henrik Leffers
;   APPLICANT: Anne Mette Buhl Hertz
;   APPLICANT: Jorgen Kjems
;   TITLE OF INVENTION: Methods and kits for diagnosing and
;   TITLE OF INVENTION: treating B-cell Chronic lymphocytic leukemia (B-CLL)
;   FILE REFERENCE: P34546US01
;   CURRENT APPLICATION NUMBER: US/10/535,500A

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; CURRENT FILING DATE:      2005-05-18          10535500-11_vs_10535500allna.txt
; PRIOR APPLICATION NUMBER: DK/PA 200201792
; PRIOR FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
;   LENGTH: 89650
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: human genome sequence
US-10-535-500A-5

Query Match        2.2%;   Score 207.8; DB 1;  Length 89650;
Best Local Similarity   76.7%;   Pred. No. 0.023;
Matches  254;  Conservative   0;  Mismatches   77;  Indels   0;  Gaps   0;

Qy    4519 TACATCTTGTCTATTATAAAAAGACTGGTTTTGGCAGGTGGTGGCTCACACCTGTAA 4578
                ||  ||||||    |||      |||||| |||||||||||||| ||||||||
Db   85190 TAACTTTTTTAAAGAAAATATATTTTTGGCTAGTTGTGGTGGCTCATGCCTGTAA 85131

Qy    4579 TTCCAGCACTTTGGGAGGCCAAGGCGGGCGGGATCACCTGAGATCAGGAGTTCAGGACCAG 4638
           ||||||||||| ||||| || |||| ||||||||||| |||| |||||| ||   |||||
Db   85130 TCCCAGCACTGTGGGGATGCTGAGGCAGGCGGATCACCTGAGGTCAGGAATTGAGACCAG 85071

Qy    4639 CCTGATCAATATGGTGAAACCCAGTCTTTACTGAAAATACAAAAATCACCCGGGTGTGGT 4698
           |||| |||| |||||||||| || ||| ||| |||||||||||| || |||||||||||
Db   85070 CCTGGGCAATGTGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGT 85011

Qy    4699 GACGGGCGCCTGTAGTCCCAGCTACTCGGGTAGCTGAGGCAGGAGAATCACTTGAACTCA 4758
           || ||||| |||||||||||| || || | || || |||||||| ||||| |||||||
Db   85010 GGCGGGTGCCTGTGTCATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCTG 84951

Qy    4759 GGAGTCAGAGGTTGCAGTGAGCTGAGATCATGCCACTGCACTCCAGCCTGGGTGACAGAG 4818
           ||||  |||||||||||  |||| ||| |  || |||||||||||||| ||  ||| ||
Db   84950 GGAGGCAGAGGTTGCAGTGAGCCAAGATGGCGCCACTGCACTCCAGCCTTGGCGATAGAG 84891

Qy    4819 CAAGACTCCATCTCAAAAAAAAAAAAAA 4849
           ||||||| | ||| |  ||||| ||| |
Db   84890 TGAGACTCCGTCTTAATAATGAAAAAATATA 84860

Search completed: October 30, 2007, 14:50:32
Job time : 303 secs
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